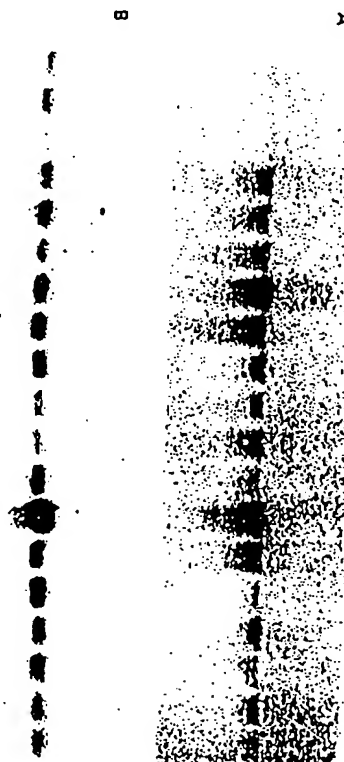


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(54) Title: GENES AMPLIFIED IN CANCER CELLS			
(57) Abstract			
<p>New methods are disclosed for detecting cancer associated genes, and obtaining corresponding cDNA sequences. The methods involve supplying RNA preparations from control cells, and from a plurality of different cancer cells that share a duplicated or deleted gene in the same region of a chromosome. Amplified cDNA copies are displayed, and then selected based on differences in abundance of RNA between preparations. Optional additional screening steps involve surveying panels of cancer cells using the cDNA for RNA overabundance with or without gene duplication. The identified genes can be used in turn to develop materials and techniques for diagnosing and treating the underlying cancer. Four novel genes associated with cancer have been identified. In at least about 60 % of the breast cancer cell lines tested, RNA hybridizing with the cDNAs were substantially more abundant than in normal cells. Most of the cell lines also showed a duplication of the corresponding gene, which probably contributed to the increased level of RNA in the cell. However, for each of the four genes, there were some cell lines which had RNA overabundance without gene duplication. This suggests that the gene product is sufficiently important to the cancer process that cells will use several alternative mechanisms to achieve increased expression.</p>			
			
<p>1: 415 ER 2: 640 ERNP 3: 640 ERP 4: 8T 474 5: CAMA 1 6: SKBR 3 7: 600 MPE 8: MDA-MB-361 9: MDA-MB-231 10: MDA-MB-134 11: MDA-MB-468 12: 8T 20 13: T47D 14: MDA-MB-157 15: UACC 812 16: MDA-MB-435 17: MCF 7 18: MDA-MB-453 19: DU 4475</p>			

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## GENES AMPLIFIED IN CANCER CELLS

### PRIORITY CLAIM

5           This application claims the priority benefit of the following U.S. Patent applications: 60/015,167, filed April 9, 1996; 60/019,202, filed June 6, 1996; 08/678,280, filed July 10, 1996. For purposes of prosecution in the U.S., the aforementioned applications are hereby incorporated herein by reference in their entirety.

### TECHNICAL FIELD

10           The present invention relates generally to the field of human genetics. More specifically, it relates to the identification of novel genes associated with overabundance of RNA in human cancer such as breast cancer. It pertains especially to those genes and the products thereof which may be  
15           important in diagnosis and treatment.

### BACKGROUND OF THE INVENTION

20           Cancer is a heterogeneous disease. It manifests itself in a wide variety of tissue sites, with different degrees of de-differentiation, invasiveness, and aggressiveness. Some forms of cancer are responsive to traditional modes of therapy, but many are not. For most common cancers, there is a pressing need to improve the arsenal of therapies available to provide more precise and more effective treatment in a less invasive way.

25           As an example, breast cancer has an unsatisfactory morbidity and mortality, despite presently available forms of medical intervention. Traditional clinical initiatives are focused on early diagnosis, followed by surgery and chemotherapy. Such interventions are of limited success, particularly in patients where the tumor has undergone metastasis.

30           The heterogeneous nature of cancer arises because different cancer cells achieve their growth and pathological properties by different phenotypic alterations. Alteration of gene expression is intimately related to the uncontrolled growth and de-differentiation that are hallmarks of cancer. Certain similar phenotypic alterations in turn may have a different genetic base in different tumors. Yet, the number of genes central to the malignant process must be a finite one. Accordingly, new pharmaceuticals that are tailored to specific genetic alterations in an individual tumor may be more effective.

35           There are two types of altered gene expression that take place, together or independently, in different cancer cells (reviewed by Bishop). The first type is the decreased expression of recessive genes, known as tumor suppresser genes, that apparently act to prevent malignant growth. The second type is the increased expression of dominant genes, such as oncogenes, that

act to promote malignant growth, or to provide some other phenotype critical for malignancy. Thus, alteration in the expression of either type of gene is a potential diagnostic indicator. Furthermore, a treatment strategy might seek to reinstate the expression of suppresser genes, or reduce the expression of dominant genes. The present invention is directed to identifying genes of either type,  
5 particularly those of the second type.

The most frequently studied mechanism for gene overexpression in cancer cells is sometimes referred to as amplification. This is a process whereby the gene is duplicated within the chromosomes of the ancestral cell into multiple copies. The process involves unscheduled replications of the region of the chromosome comprising the gene, followed by recombination of the  
10 replicated segments back into the chromosome (Alitalo et al.). As a result, 50 or more copies of the gene may be produced. The duplicated region is sometimes referred to as an "amplicon". The level of expression of the gene (that is, the amount of messenger RNA produced) escalates in the transformed cell in the same proportion as the number of copies of the gene that are made (Alitalo et al.).

Several human oncogenes have been described, some of which are duplicated, for example, in a significant proportion of breast tumors. A prototype is the *erbB2* gene (also known as *HER-2/neu*), which encodes a 185 kDa membrane growth factor receptor homologous to the epidermal growth factor receptor. *erbB2* is duplicated in 61 of 283 tumors (22%) tested in a recent survey (Adnane et al.). Other oncogenes duplicated in breast cancer are the *bcl* gene, duplicated  
20 in 34 out of 286 (12%); the *flg* gene, duplicated in 37 out of 297 (12%), the *myc* gene, duplicated in 43 out of 275 (16%) (Adnane et al.).

Work with other oncogenes, particularly those described for neuroblastoma, suggested that gene duplication of the proto-oncogene was an event involved in the more malignant forms of cancer, and could act as a predictor of clinical outcome (reviewed by Schwab et al. and Alitalo et al.). In breast cancer, duplication of the *erbB2* gene has been reported as correlating both with  
25 reoccurrence of the disease and decreased survival times (Slamon et al.). There is some evidence that *erbB2* helps identify tumors that are responsive to adjuvant chemotherapy with cyclophosphamide, doxorubicin, and fluorouracil (Muss et al.).

It is clear that only a proportion of the genes that can undergo gene duplication in cancer  
30 have been identified. First, chromosome abnormalities, such as double minute (DM) chromosomes and homogeneously stained regions (HSRs), are abundant in cancer cells. HSRs are chromosomal regions that appear in karyotype analysis with intermediate density Giemsa staining throughout their length, rather than with the normal pattern of alternating dark and light bands. They correspond to multiple gene repeats. HSRs are particularly abundant in breast cancers, showing up in 60-65% of tumors surveyed (Dutrillaux et al., Zafrani et al.). When such regions are  
35 checked by in situ hybridization with probes for any of 16 known human oncogenes, including *erbB2* and *myc*, only a proportion of tumors show any hybridization to HSR regions. Furthermore, only a proportion of the HSRs within each karyotype are implicated.



Second, comparative genomic hybridization (CGH) has revealed the presence of copy number increases in tumors, even in chromosomal regions outside of HSRs. CGH is a new method in which whole chromosome spreads are stained simultaneously with DNA fragments from normal cells and from cancer cells, using two different fluorochromes. The images are  
5 computer-processed for the fluorescence ratio, revealing chromosomal regions that have undergone amplification or deletion in the cancer cells (Kallioniemi et al. 1992). This method was recently applied to 15 breast cancer cell lines (Kallioniemi et al. 1994). DNA sequence copy number increases were detected in all 23 chromosome pairs.

Cloning the genes that undergo duplication in cancer is a formidable challenge. In one  
10 approach, human oncogenes have been identified by hybridizing with probes for other known growth-promoting genes, particularly known oncogenes in other species. For example, the *erbB2* gene was identified using a probe from a chemically induced rat neuroglioblastoma (Slamon et al.). Genes with novel sequences and functions will evade this type of search. In another approach, genes may be cloned from an area identified as containing a duplicated region by CGH method.  
15 Since CGH is able to indicate only the approximate chromosomal region of duplicated genes, an extensive amount of experimentation is required to walk through the entire region and identify the particular gene involved.

Genes may also be overexpressed in cancer without being duplicated. Methods that rely on identification from genetic abnormalities necessarily bypass such genes. Increased expression  
20 can come about through a higher level of transcription of the gene; for example, by up-regulation of the promoter or substitution with an alternative promoter. It can also occur if the transcription product is able to persist longer in the cell; for example, by increasing the resistance to cytoplasmic RNase or by reducing the level of such cytoplasmic enzymes. Two examples are the epidermal growth factor receptor, overexpressed in 45% of breast cancer tumors (Klijn et al.), and the IGF-1  
25 receptor, overexpressed in 50-93% of breast cancer tumors (Berns et al.). In almost all cases, the overexpression of each of these receptors is by a mechanism other than gene duplication.

One way of examining overexpression at the messenger RNA level is by subtractive hybridization. It involves producing positive and negative cDNA strands from two RNA preparations, and looking for cDNA which is not completely hybridized by the opposing preparation.  
30 This is a laborious procedure which has distinct limitations in cancer research. In particular, since each subtraction involves cDNA from only two cell populations at a time, it is sensitive to individual phenotypic differences due not just to the presence of cancer, but also through natural metabolic variations.

Another way of examining overexpression at the messenger RNA level is by differential  
35 display (Liang et al. 1992a). In this technique, cDNA is prepared from only a subpopulation of each RNA preparation, and expanded via the polymerase chain reaction using primers of particular specificity. Similar subpopulations are compared across several RNA preparations by gel autoradiography for expression differences. In order to survey the RNA preparations entirely, the assay is repeated with a comprehensive set of PCR primers. The screening strategy more

effectively includes multiple positive and negative control samples (Sunday et al.). The method has recently been applied to breast cancer cell lines, and highlights a number of expression differences (Liang et al. 1992b; Chen et al., McKenzie et al., Watson et al. 1994 & 1996, Kocher et al.). By excising the corresponding region of the separating gel, it is possible to recover and sequence the cDNA.

Despite the advancement provided by differential display, problems remain in terms of applying it in the search for new cancer genes. First, because this is a test for RNA levels, any phenotypic difference between cell lines constitute part of the recovered set, leading to a large proportion of "false positive" identifications. It has been found that cDNA for mitochondrial genes constitute a large proportion of the differentially expressed bands, and it consumes substantial resources to recover the sample and obtain a partial sequence in order to eliminate them. Second, false positive identifications are made for reasons attributed to multiple cDNA species and competition for the PCR primers by RNA species of different abundance (Debouck). Third, differential display highlights high copy number mRNAs and shorter mRNAs (Bertioli et al., Yeatman et al.), and may therefore miss critical cancer-associated transcripts when used as a survey technique. Fourth, a number of adjustments are made to gene expression levels when a cell undergoes malignant transformation or cultured in vitro. Most of these adjustments are secondary, and not part of the transformation process. Thus, even when a novel sequence is obtained from the differential display, it is far from certain that the corresponding gene is at the root of the disease process.

An early step in developing gene-specific therapeutic approaches is the identification of genes that are more central to malignant transformation or the persistence of the malignant phenotype.

#### DISCLOSURE OF THE INVENTION

It is an objective of this invention to provide a method for identifying and characterizing genes and gene products which are duplicated or associated with overabundant RNA in cancer cells. The method can be used for any type of cancer, providing a plurality of cell populations or cell lines of the type of cancer are available, in conjunction with a suitable control cell population. The method is highly effective in identifying genes and gene products that are intimately related to malignant transformation or maintenance of the malignant properties of the cancer cells.

An important derivative of applying the method is the selection and retrieval of cDNA and cDNA fragments corresponding to the cancer-associated gene. These fragments can be used *inter alia* to determine the nucleotide sequence of the gene and mRNA, the amino acid sequence of any encoded protein, or to retrieve from a cDNA or genomic library additional polynucleotides related to the gene or its transcripts. Since the genes are typically involved in the malignant

process of the cell, the polynucleotides, polypeptides, and antibodies derived by using this method can in turn be used to design or screen important diagnostic reagents and therapeutic compounds.

Another objective of this invention to provide isolated polynucleotides, polypeptides, and antibodies derived from four novel genes which are associated with several different types of cancer, including breast cancer. The genes are designated CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1. These designations refer to both strands of the cDNA and fragments thereof; and to the respective corresponding messenger RNA, including splice variants, allelic variants, and fragments of any of these forms. These genes show RNA overabundance in a majority of cancer cell lines tested. A majority of the cells showing RNA overabundance also have duplication of the corresponding gene. Another object of this invention is to provide materials and methods based on these polynucleotides, polypeptides, and antibodies for use in the diagnosis and treatment of cancer, particularly breast cancer.

Accordingly, one embodiment of this invention is an isolated polynucleotide comprising a linear sequence contained in a polynucleotide selected from the group consisting of CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1. The linear sequence is contained in a duplicated gene or overabundant RNA in cancerous cells. The RNA may be overabundant due to gene duplication, increased RNA transcription or processing, increased RNA persistence, any combination thereof, or by any other mechanism, in a proportion of breast cancer cells. Preferably, the RNA is overabundant in at least about 20% of a representative panel of breast cancer cell lines, such as the panels listed herein; more preferably, it is overabundant in at least about 40% of the panel; even more preferably, it is overabundant in at least 60% or more of the panel. Preferably, the RNA is overabundant in at least about 5% of spontaneously occurring breast cancer tumors; more preferably, it is overabundant in at least about 10% of such tumors; more preferably, it is overabundant in at least about 20% of such tumors; more preferably, it is overabundant in at least about 30% of such tumors; even more preferably, it is overabundant in at least about 50% of such tumors.

Preferably, a sequence of at least 10 nucleotides is essentially identical between the isolated polynucleotide of the invention and a cDNA from CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1; more preferably, a sequence of at least about 15 nucleotides is essentially identical; more preferably, a sequence of at least about 20 nucleotides is essentially identical; more preferably, a sequence of at least about 30 nucleotides is essentially identical; more preferably, a sequence of at least about 40 nucleotides is essentially identical; even more preferably, a sequence of at least about 70 nucleotides is essentially identical; still more preferably, a sequence of about 100 nucleotides or more is essentially identical. A further embodiment of this invention is an isolated polynucleotide comprising a linear sequence essentially identical to a sequence selected from the group consisting of SEQ. ID NO:15, SEQ. ID NO:18, SEQ. ID NO:21, SEQ. ID NO:23, SEQ. ID NO:26, SEQ. ID NO:29, SEQ. ID NO:31, SEQ. ID NO:33, and SEQ. ID NO:35. These embodiments include an isolated polynucleotide which is a DNA polynucleotide, an RNA polynucleotide, a polynucleotide probe, or a polynucleotide primer.

This invention also provides an isolated polypeptide comprising a sequence of amino acids essentially identical to the polypeptide encoded by or translated from a polynucleotide selected from the group consisting of CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1. Preferably, a sequence of at least about 5 amino acids is essentially identical between the polypeptide of this invention and that encoded by the polynucleotide; more preferably, a sequence of at least about 10 amino acids is essentially identical; more preferably, a sequence of at least 15 amino acids is essentially identical; even more preferably, a sequence of at least 20 amino acids is essentially identical; still more preferably, a sequence of about 30 amino acids or more is essentially identical. Preferably, the polypeptide comprises a linear sequence of at least 15 amino acids essentially identical to a sequence encoded by said polynucleotide. Another embodiment of this invention is a polypeptide comprising a linear sequence essentially identical to a sequence selected from the group consisting of SEQ. ID NO:17, SEQ. ID NO:20, SEQ. ID NO:25, SEQ. ID NO:28, SEQ. ID NO:30, SEQ. ID NO:32, SEQ. ID NO:34; and SEQ. ID NO:37.

A further embodiment of this invention is an antibody specific for a polypeptide embodied in this invention. This encompasses both monoclonal and isolated polyclonal antibodies.

A further embodiment of this invention is a method of using the polynucleotides of this invention for detecting or measuring gene duplication in cancerous cells, especially but not limited to breast cancer cells, comprising the steps of reacting DNA contained in a clinical sample with a reagent comprising the polynucleotide, said clinical sample having been obtained from an individual suspected of having cancerous cells; and comparing the amount of complexes formed between the reagent and the DNA in the clinical sample with the amount of complexes formed between the reagent and DNA in a control sample.

A further embodiment is a method of using the polynucleotides of this invention for detecting or measuring overabundance of RNA in cancerous cells, especially but not limited to breast cancer cells, comprising the steps of reacting RNA contained in a clinical sample with a reagent comprising the polynucleotide, said clinical sample having been obtained from an individual suspected of having cancerous cells; and comparing the amount of complexes formed between the reagent and the RNA in the clinical sample with the amount of complexes formed between the reagent and RNA in a control sample.

Another embodiment of this invention is a diagnostic kit for detecting or measuring gene duplication or RNA overabundance in cells contained in an individual as manifest in a clinical sample, comprising a reagent and a buffer in suitable packaging, wherein the reagent comprises a polynucleotide of this invention.

Another embodiment of this invention is a method of using a polypeptide of this invention for detecting or measuring specific antibodies in a clinical sample, comprising the steps of reacting antibodies contained in the clinical sample with a reagent comprising the polypeptide, said clinical sample having been obtained from an individual suspected of having cancerous cells, especially but not limited to breast cancer cells; and comparing the amount of complexes formed between the

reagent and the antibodies in the clinical sample with the amount of complexes formed between the reagent and antibodies in a control sample.

Another embodiment of this invention is a method of using an antibody of this invention for detecting or measuring altered protein expression in a clinical sample, comprising the steps of  
5 reacting a polypeptide contained in the clinical sample with a reagent comprising the antibody, said clinical sample having been obtained from an individual suspected of having cancerous cells, especially but not limited to breast cancer cells; and comparing the amount of complexes formed between the reagent and the polypeptide in the clinical sample with the amount of complexes formed between the reagent and a polypeptide in a control sample. Further embodiments of this invention  
10 are diagnostic kits for detecting or measuring a polypeptide or antibody present in a clinical sample, comprising a reagent and a buffer in suitable packaging, wherein the reagent respectively comprises either an antibody or a polypeptide of this invention.

Yet another embodiment of this invention is a host cell transfected by a polynucleotide of this invention. A further embodiment of this invention is a method for using a polynucleotide for screening  
15 a pharmaceutical candidate, comprising the steps of separating progeny of the transfected host cell into a first group and a second group; treating the first group of cells with the pharmaceutical candidate; not treating the second group of cells with the pharmaceutical candidate; and comparing the phenotype of the treated cells with that of the untreated cells.

This invention also embodies a pharmaceutical preparation for use in cancer therapy,  
20 comprising a polynucleotide or polypeptide embodied by this invention, said preparation being capable of reducing the pathology of cancerous cells, especially for but not limited to breast cancer cells. Further embodiments of this invention are methods for treating an individual bearing cancerous cells, such as breast cancer cells, comprising administering any of the aforementioned pharmaceutical preparations.

25 Still another embodiment of this invention is a pharmaceutical preparation or active vaccine comprising a polypeptide embodied by this invention in an immunogenic form and a pharmaceutically compatible excipient. A further embodiment is a method for treatment of cancer, especially but not limited to breast cancer, either prophylactically or after cancerous cells are present in an individual being treated, comprising administration of the aforementioned pharmaceutical preparation.

30 Another series of embodiments of this invention relate to methods for obtaining cDNA corresponding to a gene associated with cancer, comprising the steps of: a) supplying an RNA preparation from uncultured control cells; b) supplying RNA preparations from at least two different cancer cells; c) displaying cDNA corresponding to the RNA preparations of step a) and step b) such that different cDNA corresponding to different RNA in each preparation are displayed  
35 separately; d) selecting cDNA corresponding to RNA that is present in greater abundance in the cancer cells of step b) relative to the control cells of step a); e) supplying a digested DNA preparation from control cells; f) supplying digested DNA preparations from at least two different cancer cells; g) hybridizing the cDNA of step d) with the digested DNA preparations of step e) and

step f); and h) further selecting cDNA from the cDNA of step d) corresponding to genes that are duplicated in the cancer cells of step f) relative to the control cells of step e).

One or more enhancements may optionally be included in the methods of this invention, including the following:

- 5           1. Cancer cells are preferably used for step b) that share a duplicated gene in the same region of a chromosome. If desired, the practitioner may test cancer cells beforehand to detect the duplication or deletion of chromosome regions; or cancer cell lines may be used that have already been characterized in this respect.
- 10           2. A higher plurality of cancer cells are preferably used to provide DNA for step b), step f), or preferably both step b) and step f). The use of three cancer cells is preferred over two; the use of four cancer cells is more preferred, about five cancer cells is still more preferred, about eight cancer cells is even more preferred. The cDNA of each cancer cell population is displayed or hybridized separately, in accordance with the method.
- 15           3. A higher plurality of control cells are preferably used to provide DNA for step a), step e), or preferably both step a) and step e). The use of two control cell populations is preferred; the use of three or more is even more preferred. Both proliferating and non-proliferating populations are preferably used, if available.
- 20           4. The control cells are preferably supplied fresh from a tissue source, and are not cultured or transformed into a cell line. This is increasingly important when the control cell populations used in step a) is only one or two in number. Freshly obtained cancer cells may also be used as an alternative to cancer cell lines, although this is less critical.
- 25           5. An additional screening step is preferably conducted in which the cDNA corresponding to the putative cancer-associated gene is additionally hybridized with a digested mitochondrial DNA preparation, to eliminate mitochondrial genes. This screening step may be conducted before, between, subsequent to, or simultaneously with the other screening steps of the method.
- 30           6. An additional screening step is preferably conducted in which RNA is supplied from a plurality of cancer cells, and one or preferably more control cell populations; the RNA is contacted with cDNA corresponding to the putative cancer-associated gene under conditions that permit formation of a stable duplex, and cDNA is selected corresponding to RNA that is present in greater abundance in a proportion of the cancer cells relative to the control cells. Preferably, the plurality of cancer cells is a panel of at least five, preferably at least ten cells. Preferably at least three, more preferably at least five of the cancer cells show greater abundance of RNA. Preferably at least one and preferably more of the cancer cells shows a greater abundance of RNA compared with control cells, but does not show duplication of the corresponding gene in step h) of the method.
- 35

Other embodiments of the invention are methods for obtaining cDNA corresponding to a gene that is deleted or underexpressed in cancer, comprising the steps of: a) supplying an RNA preparation from control cells; b) supplying RNA preparations from at least two different cancer cells that share a deleted gene in the same region of a chromosome; c) displaying cDNA  
5 corresponding to the RNA preparations of step a) and step b) such that different cDNA corresponding to different RNA in each preparation are displayed separately; and d) selecting cDNA corresponding to RNA that is present in lower abundance in the cancer cells of step b) relative to the control cells of step a). Such methods typically comprise the following further steps: e) supplying a digested DNA preparation from control cells; f) supplying digested DNA  
10 preparations from at least two different cancer cells; g) hybridizing the cDNA of step d) with the digested DNA preparations of step e) and step f); and h) further selecting cDNA from the cDNA of step d) corresponding to a gene that is deleted in the cancer cells of step f) relative to the control cells of step e). Such methods for identifying deleted or underexpressed genes may also comprise enhancements such as those described above.

15 Additional embodiments of this invention are methods for characterizing cancer genes, comprising obtaining cDNA corresponding to a cancer-associated gene according to a method of this invention, particularly those highlighted above, and then sequencing the cDNA. Alternatively or in addition, the cDNA may be used to rescue additional polynucleotides corresponding to a cancer-associated gene from an mRNA preparation, or a cDNA or genomic DNA library.

20 Additional embodiments of this invention are methods for screening candidate drugs for cancer treatment, comprising obtaining cDNA corresponding to a gene that is duplicated, overexpressed, deleted, or underexpressed in cancer, and comparing the effect of the candidate drug on a cell genetically altered with the cDNA or fragment thereof with the effect on a cell not genetically altered.

25 Various embodiments of this invention may be employed in pursuit of any form of cancer for which suitable tissue sources are available. Cancers of particular interest include lung cancer, glioblastoma, pancreatic cancer, colon cancer, prostate cancer, hepatoma, myeloma, and breast cancer.

### 30 **BRIEF DESCRIPTION OF THE DRAWINGS**

**Figure 1** is a half-tone reproduction of an autoradiogram of a differential display experiment, in which radiolabeled cDNA corresponding to a subset of total messenger RNA in different cells are compared. This is used to select cDNA corresponding to particular RNA that are overabundant in breast cancer.

35 **Figure 2** is a half-tone reproduction of an autoradiogram of electrophoresed DNA digests from a panel of breast cancer cell lines probed with a CH8-2a13-1 insert (Panel A) or a loading control (Panel B).

**Figure 3** is a half-tone reproduction of an autoradiogram of electrophoresed total RNA from a panel of breast cancer cell lines probed with a CH8-2a13-1 insert (Panel A) or a loading control (Panel B).

5 **Figure 4** is a half-tone reproduction of an autoradiogram of electrophoresed DNA digests from a panel of breast cancer cell lines probed with a CH13-2a12-1 insert.

**Figure 5** is a half-tone reproduction of an autoradiogram of electrophoresed total RNA from a panel of breast cancer cell lines probed with a CH13-2a12-1 insert.

10

**Figure 6** is a map of cDNA fragments obtained for the breast cancer associated genes CH1-9a11-2, CH8-2a13-1, CH13-2a12-1 and CH14-2a16-1. Regions of the fragments used to deduce sequence data listed in the application are indicated by shading. Nucleotide positions are numbered from the left-most residue for which double-strand sequence data has been obtained, which is not necessarily the 5' terminus of the corresponding message.

15

**Figure 7** is a listing of primers used for obtaining the cDNA sequence data for CH1-9a11-2.

**Figure 8** is a listing of cDNA sequence obtained for CH1-9a11-2.

20

**Figure 9** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH1-9a11-2 shown in Figure 8. The single-letter amino acid code is used. Stop codons are indicated by a dot (●). The upper panel shows the complete amino acid translation; the lower panel shows the predicted gene product protein sequence. A possible transmembrane region is indicated by underlining.

25

**Figure 10** is a listing of primers used for obtaining the cDNA sequence data for CH8-2a13-1.

**Figure 11** is a listing of cDNA sequence obtained for CH8-2a13-1.

30

**Figure 12** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH8-2a13-1 shown in Figure 11. The upper panel shows the complete amino acid translation; the lower panel shows the predicted gene product protein sequence.

35 **Figure 13** is a listing of the nucleotide sequence predicted for a full-length CH8-2a13-1 cDNA.

**Figure 14** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH8-2a13-1 shown in Figure 13.



**Figure 15** is a listing of primers used for obtaining the cDNA sequence data for CH13-2a12-1.

**Figure 16** is a listing of cDNA sequence obtained for CH13-2a12-1.

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**Figure 17** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH13-2a12-1 shown in Figure 16. The upper panel shows the complete amino acid translation; the lower panel shows the predicted gene product protein sequence.

10 **Figure 18** is a listing of primers used for obtaining cDNA sequence data for CH13-2a12-1..

**Figure 19** is a listing of the cDNA sequence data obtained by two-directional sequencing for CH14-2a16-1.

15 **Figure 20** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH14-2a16-1 shown in Figure 19. The upper panel shows the complete amino acid translation; the lower panel shows the predicted gene product protein sequence. Residues corresponding to three zinc finger motifs are underlined, indicating that the protein may have DNA or RNA binding activity.

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**Figure 21** is a listing of additional DNA sequence data towards the 5' end of CH14-2a16-1 obtained by one-directional sequencing of the fragment pCH14-1.3. First two panels show nucleotide and amino acid sequence from the 5' end of the fragment; the second two panels show nucleotide and amino acid sequence from the 3' end of the fragment. Regions of overlap with pCH14-800 are underlined.

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**Figure 22** is a listing of the nucleotide sequences of initial fragments obtained corresponding to the four breast cancer associated genes, along with their amino acid translations.

30 **Figure 23** is a listing of additional cDNA sequence obtained for CH1-9a11-2, comprising approximately 1934 base pairs 5' from the sequence of Figure 8.

**Figure 24** is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH1-9a11-2 shown in Figure 23. The single-letter amino acid code is used.

35 Stop codons are indicated by a dot (●).

**Figure 25** is a listing of additional cDNA sequence obtained for CH14-2a16-1, comprising approximately 1934 base pairs 5' from the sequence of Figure 19.

*Figure 26* is a listing of the amino acid sequence corresponding to the longest open reading frame of the DNA sequence of CH1-9a11-2 shown in Figure 25. The single-letter amino acid code is used. Stop codons are indicated by a dot (●). The upper panel shows the complete amino acid translation; the lower panel shows the predicted gene product protein sequence.

### **BEST MODE FOR CARRYING OUT THE INVENTION**

This invention relates to the discovery and characterization of four novel genes associated with breast cancer. The cDNA of these genes, and their sequences as disclosed below, provide the basis of a series of reagents that can be used in diagnosis and therapy.

Using a panel of about 15 cancer cell lines, each of the four genes was found to be duplicated in 40-60% of the cells tested. Surprisingly, each of the four genes was duplicated in at least one cell line where studies using comparative genomic hybridization had not revealed any amplification of the corresponding chromosomal region.

Levels of expression at the mRNA level were tested in a similar panel for two of these four genes. In addition to those cell lines showing gene duplication, 17 to 37% of the lines showed RNA overabundance without gene duplication, indicating that the malignant cells had used some mechanism *other than gene duplication* to promote the abundance of RNA corresponding to these genes. All four of the breast cancer genes have open reading frames, and likely are transcribed at various levels in different cell types. Overabundance of the corresponding RNA in a cancerous cell is likely associated with overexpression of the protein gene product. Such overexpression may be manifest as increased secretion of the protein from the cell into blood or the surrounding environment, an increased density of the protein at the cell surface, or an increased accumulation the protein within the cell, in comparison to the typical level in noncancerous cells of the same tissue type.

Different tumors bear different genotypes and phenotypes, even when derived from the same tissue. Gene therapy in cancer is more likely to be effective if it is aimed at genes that are involved in supporting the malignancy of the cancer. This invention discloses genes that achieve RNA overabundance by several mechanisms, because they are more likely to be directly involved in the pathogenic process, and therefore suitable targets for pharmacological manipulation.

Features of the four novel genes, the respective mRNA, and the cDNA used to find them are provided in Table 1.

TABLE 1: Characteristics of 4 Novel Breast Cancer Genes			
Chromosome	Designation	mRNA Observed	Exemplary cDNA Fragments Cloned
1	CH1-9a11-2	5.5kb, 4.5kb	1.1 kb, 2.5 kb
8	CH8-2a13-1	4.2kb	0.6 kb (two), 3.0 kb, 4.0 kb
13	CH13-2a12-1	3.5kb, 3.2kb	1.6 kb, 3.5 kb
14	CH14-2a16-1	3.8kb, 3kb	0.8 kb, 1.3 kb, 1.6 kb, 2.5 kb

All four genes sequences are unrelated to other genes known to be overexpressed in breast cancer, including the *erbB2* gene (Adnane et al.), tissue factor (Chen et al.), mammaglobulin (Watson et al.), and *DD96* (Kocher et al.).

5 The four mRNA sequences each comprise an open reading frame. The CH1-9a11-2 gene is expressed at the mRNA level at relatively elevated levels in pancreas and testis. The CH8-2a13-1 gene is expressed at relatively elevated levels in adult heart, spleen, thymus, small intestine, colon, and tissues of the reproductive system; and at higher levels in certain tissues of the fetus. The CH13-2a12-1 gene is expressed at relatively elevated levels in heart, skeletal muscle, and testis. The CH14-2a16-1 gene is expressed at relatively elevated levels in testis. The level of expression of all four genes is especially high in a substantial proportion of breast cancer cell lines.

The CH1-9a11-2 gene encodes a protein with a putative transmembrane region, and may be expressed as a surface protein on cancer cells. The CH13-2a12-1 gene is distantly related to a *C. elegans* gene implicated in cell cycle regulation, and may play a role in the regulation of cell proliferation. The protein encoded by CH13-2a12-1 is distantly related to a vasopressin-activated calcium binding receptor, and may have  $Ca^{++}$  binding activity. The CH14-2a16-1 comprises at least five domains of a zinc finger binding motif and is distantly related to a yeast RNA binding protein. The CH14-2a16-1 gene product is suspected of having DNA or RNA binding activity, which may relate to a role in cancer pathogenesis.

20 The four genes described here are exemplars of genes that undergo altered expression in cancer, identifiable using the gene screening methods of the invention. The method involves an analysis for both DNA duplication and altered RNA abundance relating to the same gene. Since abnormal gene regulation is central to the malignant process, the identification method may be brought to bear on any type of cancer.

25 The screening method is superior to any previously available approach in several respects. Particularly significant is that screening is rapidly focused towards genes that are central to the malignant process, and away from those that have variable levels of expression as part of normal

metabolic processes. Furthermore, because the end-product is a cDNA corresponding to the gene, the process leads rapidly to detailed characterization of the gene, and any effector molecule it may encode. This in turn leads to development of new diagnostic and therapeutic materials and techniques.

5

### **Definitions**

Terms used in this application include the following:

The term "polynucleotide" refers to a polymeric form of nucleotides of any length, either  
10 deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence,  
15 nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

20 The term polynucleotide, as used herein, refers interchangeably to double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form, and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

In the context of polynucleotides, a "linear sequence" or a "sequence" is an order of  
25 nucleotides in a polynucleotide in a 5' to 3' direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polynucleotide. A "partial sequence" is a linear sequence of part of a polynucleotide which is known to comprise additional residues in one or both directions.

"Hybridization" refers to a reaction in which one or more polynucleotides react to form a  
30 complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding is sequence-specific, and typically occurs by Watson-Crick base pairing. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of a PCR, or the enzymatic cleavage of a polynucleotide by a ribozyme.

Hybridization reactions can be performed under conditions of different "stringency". Relevant  
35 conditions include temperature, ionic strength, time of incubation, the presence of additional solutes in the reaction mixture such as formamide, and the washing procedure. Higher stringency conditions are those conditions, such as higher temperature and lower sodium ion concentration, which require higher minimum complementarity between hybridizing elements for a stable hybridization complex to form. Conditions that increase the stringency of a hybridization reaction are widely known and

published in the art: see, for example, "Molecular Cloning: A Laboratory Manual", Second Edition (Sambrook, Fritsch & Maniatis, 1989).

When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, those polynucleotides are described as "complementary". A double-stranded polynucleotide can be "complementary" to another polynucleotide, if hybridization can occur between one of the strands of the first polynucleotide and the second. Complementarity (the degree that one polynucleotide is complementary with another) is quantifiable in terms of the proportion of bases in opposing strands that are expected to form hydrogen bonding with each other, according to generally accepted base-pairing rules.

A linear sequence of nucleotides is "identical" to another linear sequence, if the order of nucleotides in each sequence is the same, and occurs without substitution, deletion, or material substitution. It is understood that purine and pyrimidine nitrogenous bases with similar structures can be functionally equivalent in terms of Watson-Crick base-pairing; and the inter-substitution of like nitrogenous bases, particularly uracil and thymine, or the modification of nitrogenous bases, such as by methylation, does not constitute a material substitution. An RNA and a DNA polynucleotide have identical sequences when the sequence for the RNA reflects the order of nitrogenous bases in the polyribonucleotides, the sequence for the DNA reflects the order of nitrogenous bases in the polydeoxyribonucleotides, and the two sequences satisfy the other requirements of this definition. Where one or both of the polynucleotides being compared is double-stranded, the sequences are identical if one strand of the first polynucleotide is identical with one strand of the second polynucleotide.

A linear sequence of nucleotides is "essentially identical" to another linear sequence, if both sequences are capable of hybridizing to form a duplex with the same complementary polynucleotide. Sequences that hybridize under conditions of greater stringency are more preferred. It is understood that hybridization reactions can accommodate insertions, deletions, and substitutions in the nucleotide sequence. Thus, linear sequences of nucleotides can be essentially identical even if some of the nucleotide residues do not precisely correspond or align. In general, essentially identical sequences of about 40 nucleotides in length will hybridize at about 300C in 10 x SSC (0.15 M NaCl, 15 mM citrate buffer); preferably, they will hybridize at about 400C in 6 x SSC; more preferably, they will hybridize at about 500C in 6 x SSC; even more preferably, they will hybridize at about 600C in 6 x SSC, or at about 400C in 0.5 x SSC, or at about 300C in 6 x SSC containing 50% formamide; still more preferably, they will hybridize at 400C or higher in 2 x SSC or lower in the presence of 50% or more formamide. It is understood that the rigor of the test is partly a function of the length of the polynucleotide; hence shorter polynucleotides with the same homology should be tested under lower stringency and longer polynucleotides should be tested under higher stringency, adjusting the conditions accordingly. The relationship between hybridization stringency, degree of sequence identity, and polynucleotide length is known in the art and can be calculated by standard formulae; see, e.g., Meinkoth et al. Sequences that correspond or align more closely to the invention disclosed herein are comparably more preferred. Generally, essentially identical sequences are at least about

50% identical with each other, after alignment of the homologous regions. Preferably, the sequences are at least about 60% identical; more preferably, they are at least about 70% identical; more preferably, they are at least about 80% identical; more preferably, the sequences are at least about 90% identical; even more preferably, they are at least 95% identical; still more preferably, the sequences are 100% identical. Percent identity is calculated as the percent of residues in the sequence being compared that are identical to those in the reference sequence, which is usually one of those listed or described in this application, unless stated otherwise. No penalty is imposed for introduction of gaps in the reference or comparison sequence for purposes of alignment, but the resulting fragments must be rationally derived — small gaps may not be introduced to trivially improve the identity score.

In determining whether polynucleotide sequences are essentially identical, a sequence that preserves the functionality of the polynucleotide with which it is being compared is particularly preferred. Functionality may be established by different criteria, such as ability to hybridize with a target polynucleotide, and whether the polynucleotide encodes an identical or essentially identical polypeptides. Thus, nucleotide substitutions which cause a non-conservative substitution in the encoded polypeptide are preferred over nucleotide substitutions that create a stop codon; nucleotide substitutions that cause a conservative substitution in the encoded polypeptide are more preferred, and identical nucleotide sequences are even more preferred. Insertions or deletions in the polynucleotide that result in insertions or deletions in the polypeptide are preferred over those that result in the down-stream coding region being rendered out of phase. The relative importance of hybridization properties and the polypeptide encoded by a polynucleotide depends on the application of the invention.

A "reagent" polynucleotide, polypeptide, or antibody, is a substance provided for a reaction, the substance having some known and desirable parameters for the reaction. A reaction mixture may also contain a "target", such as a polynucleotide, antibody, or polypeptide that the reagent is capable of reacting with. For example, in some types of diagnostic tests, the amount of the target in a sample is determined by adding a reagent, allowing the reagent and target to react, and measuring the amount of reaction product. In the context of clinical management, a "target" may also be a cell, collection of cells, tissue, or organ that is the object of an administered substance, such as a pharmaceutical compound.

"cDNA" or "complementary DNA" is a single- or double-stranded DNA polynucleotide in which one strand is complementary to a messenger RNA. "Full-length cDNA" is cDNA comprised of a strand which is complementary to an entire messenger RNA molecule. A "cDNA fragment" as used herein generally represents a sub-region of the full-length form, but the entire full-length cDNA may also be included. Unless explicitly specified, the term cDNA encompasses both the full-length form and the fragment form.

Different polynucleotides are said to "correspond" to each other if one is ultimately derived from another. For example, messenger RNA corresponds to the gene from which it is transcribed. cDNA corresponds to the RNA from which it has been produced, such as by a reverse transcription

reaction, or by chemical synthesis of a DNA based upon knowledge of the RNA sequence. cDNA also corresponds to the gene that encodes the RNA. Polynucleotides may be said to correspond even when one of the pair is derived from only a portion of the other.

5 A "probe" when used in the context of polynucleotide manipulation refers to a polynucleotide which is provided as a reagent to detect a target potentially present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and enzymes.

10 A "primer" is a short polynucleotide, generally with a free 3' -OH group, that binds to a target potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target. A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made of a target polynucleotide using one or more primers, and a catalyst of polymerization, such as a reverse transcriptase or a DNA polymerase, and particularly a thermally stable polymerase enzyme. Methods for PCR are taught in U.S. Patent Nos.  
15 4,683,195 (Mullis) and 4,683,202 (Mullis et al.). All processes of producing replicate copies of the same polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "replication."

An "operon" is a genetic region comprising a gene encoding a protein and functionally related 5' and 3' flanking regions. Elements within an operon include but are not limited to promoter regions, enhancer regions, repressor binding regions, transcription initiation sites, ribosome binding sites,  
20 translation initiation sites, protein encoding regions, introns and exons, and termination sites for transcription and translation. A "promoter" is a DNA region capable under certain conditions of binding RNA polymerase and initiating transcription of a coding region located downstream (in the 3' direction) from the promoter. "Operably linked" refers to a juxtaposition of genetic elements, wherein the elements are in a relationship permitting them to operate in the expected manner. For instance, a  
25 promoter is operably linked to a coding region if the promoter helps initiate transcription of the coding sequence. There may be intervening residues between the promoter and coding region so long as this functional relationship is maintained.

"Gene duplication" is a term used herein to describe the process whereby an increased number of copies of a particular gene or a fragment thereof is present in a particular cell or cell line.

30 "Gene amplification" generally is synonymous with gene duplication.

"Expression" is defined alternately in the scientific literature either as the transcription of a gene into an RNA polynucleotide, or as the transcription and subsequent translation into a polypeptide. As used herein, "expression" or "gene expression" generally refers to the production of the RNA unless specified or required otherwise. Thus, "RNA overexpression" reflects the presence of  
35 more RNA (as a proportion of total RNA) from a particular gene in a cell being described, such as a cancerous cell, in relation to that of the cell it is being compared with, such as a non-cancerous cell. The protein product of the gene may or may not be produced in normal or abnormal amounts. "Protein overexpression" similarly reflects the presence of relatively more protein present in or produced by, for example, a cancerous cell.

"Abundance" of RNA refers to the amount of a particular RNA present in a particular cell type.

Thus, "RNA overabundance" or "overabundance of RNA" describes RNA that is present in greater proportion of total RNA in the cell type being described, compared with the same RNA as a proportion of the total RNA in a control cell. A number of mechanisms may contribute to RNA overabundance in a particular cell type: for example, gene duplication, increased level of transcription of the gene, increased persistence of the RNA within the cell after it is produced, or any combination of these. Similarly, "lower abundance" or "underabundance" describes RNA that is present in lower proportion in the cell being described compared with a control cell.

The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation, such as conjugation with a labeling component.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an N-terminal to C-terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide which is known to comprise additional residues in one or both directions.

A linear sequence of amino acids is "essentially identical" to another sequence if the two sequences have a substantial degree of sequence identity. It is understood that the functional proteins can accommodate insertions, deletions, and substitutions in the amino acid sequence. Thus, linear sequences of amino acids can be essentially identical even if some of the residues do not precisely correspond or align. Sequences that correspond or align more closely to the invention disclosed herein are more preferred. It is also understood that some amino acid substitutions are more easily tolerated. For example, substitution of an amino acid with hydrophobic side chains, aromatic side chains, polar side chains, side chains with a positive or negative charge, or side chains comprising two or fewer carbon atoms, by another amino acid with a side chain of like properties can occur without disturbing the essential identity of the two sequences. Methods for determining homologous regions and scoring the degree of homology are well known in the art; see for example Altschul et al. and Henikoff et al. Well-tolerated sequence differences are referred to as "conservative substitutions". Thus, sequences with conservative substitutions are preferred over those with other substitutions in the same positions; sequences with identical residues at the same positions are still more preferred. In general, amino acid sequences that are essentially identical are at least about 15% identical, and comprise at least about another 15% which are either identical or are conservative substitutions, after alignment of homologous regions. More preferably, essentially identical sequences comprise at least about 50% identical residues or conservative substitutions; more preferably, they comprise at least about 70% identical residues or conservative substitutions; more preferably, they comprise at least about 80% identical residues or conservative substitutions; more



preferably, they comprise at least about 90% identical residues or conservative substitutions; more preferably, they comprise at least about 95% identical residues or conservative substitutions; even more preferably, they contain 100% identical residues.

5 In determining whether polypeptide sequences are essentially identical, a sequence that preserves the functionality of the polypeptide with which it is being compared is particularly preferred. Functionality may be established by different parameters, such as enzymatic activity, the binding rate or affinity in a receptor-ligand interaction, the binding affinity with an antibody, and X-ray crystallographic structure.

10 An "antibody" (interchangeably used in plural form) is an immunoglobulin molecule capable of specific binding to a target, such as a polypeptide, through at least one antigen recognition site, located in the variable region of the immunoglobulin molecule. As used herein, the term encompasses not only intact antibodies, but also fragments thereof, mutants thereof, fusion proteins, humanized antibodies, and any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site of the required specificity.

15 The term "antigen" refers to the target molecule that is specifically bound by an antibody through its antigen recognition site. The antigen may, but need not be chemically related to the immunogen that stimulated production of the antibody. The antigen may be polyvalent, or it may be a monovalent hapten. Examples of kinds of antigens that can be recognized by antibodies include polypeptides, polynucleotides, other antibody molecules, oligosaccharides, complex lipids, drugs, and  
20 chemicals. An "immunogen" is an antigen capable of stimulating production of an antibody when injected into a suitable host, usually a mammal. Compounds may be rendered immunogenic by many techniques known in the art, including crosslinking or conjugating with a carrier to increase valency, mixing with a mitogen to increase the immune response, and combining with an adjuvant to enhance presentation.

25 An "active vaccine" is a pharmaceutical preparation for human or animal use, which is used with the intention of eliciting a specific immune response. The immune response may be either humoral or cellular, systemic or secretory. The immune response may be desired for experimental purposes, for the treatment of a particular condition, for the elimination of a particular substance, or for prophylaxis against a particular condition or substance.

30 An "isolated" polynucleotide, polypeptide, protein, antibody, or other substance refers to a preparation of the substance devoid of at least some of the other components that may also be present where the substance or a similar substance naturally occurs or is initially obtained from. Thus, for example, an isolated substance may be prepared by using a purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per  
35 volume of solution, or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this invention are increasingly more preferred. Thus, for example, a 2-fold enrichment is preferred, 10-fold enrichment is more preferred, 100-fold enrichment is more preferred, 1000-fold enrichment is even more

preferred. A substance can also be provided in an isolated state by a process of artificial assembly, such as by chemical synthesis or recombinant expression.

5 A polynucleotide used in a reaction, such as a probe used in a hybridization reaction, a primer used in a PCR, or a polynucleotide present in a pharmaceutical preparation, is referred to as "specific" or "selective" if it hybridizes or reacts with the intended target more frequently, more rapidly, or with greater duration than it does with alternative substances. Similarly, an antibody is referred to as "specific" or "selective" if it binds via at least one antigen recognition site to the intended target more frequently, more rapidly, or with greater duration than it does to alternative substances. A polynucleotide or antibody is said to "selectively inhibit" or "selectively interfere with" a reaction if it 10 inhibits or interferes with the reaction between particular substrates to a greater degree or for a greater duration than it does with the reaction between alternative substrates. An antibody is capable of "specifically delivering" a substance if it conveys or retains that substance near a particular cell type more frequently or for a greater duration compared with other cell types.

The "effector component" of a pharmaceutical preparation is a component which modifies 15 target cells by altering their function in a desirable way when administered to a subject bearing the cells. Some advanced pharmaceutical preparations also have a "targeting component", such as an antibody, which helps deliver the effector component more efficaciously to the target site. Depending on the desired action, the effector component may have any one of a number of modes of action. For example, it may restore or enhance a normal function of a cell, it may eliminate or suppress an abnormal function of a cell, or it may alter a cell's phenotype. Alternatively, it may kill or render 20 dormant a cell with pathological features, such as a cancer cell. Examples of effector components are provided in a later section.

A "pharmaceutical candidate" or "drug candidate" is a compound believed to have therapeutic potential, that is to be tested for efficacy. The "screening" of a pharmaceutical candidate refers to 25 conducting an assay that is capable of evaluating the efficacy and/or specificity of the candidate. In this context, "efficacy" refers to the ability of the candidate to effect the cell or organism it is administered to in a beneficial way: for example, the limitation of the pathology of cancerous cells.

A "cell line" or "cell culture" denotes higher eukaryotic cells grown or maintained in vitro. It is understood that the descendants of a cell may not be completely identical (either morphologically, 30 genotypically, or phenotypically) to the parent cell. Cells described as "uncultured" are obtained directly from a living organism, and have been maintained for a limited amount of time away from the organism: not long enough or under conditions for the cells to undergo substantial replication.

"Genetic alteration" refers to a process wherein a genetic element is introduced into a cell other than by mitosis or meiosis. The element may be heterologous to the cell, or it may be an additional copy or improved version of an element already present in the cell. Genetic alteration 35 may be effected, for example, by transfecting a cell with a recombinant plasmid or other polynucleotide through any process known in the art, such as electroporation, calcium phosphate precipitation, or contacting with a polynucleotide-liposome complex, or by transduction or infection

with a DNA or RNA virus or viral vector. The alteration is preferably but not necessarily inheritable by progeny of the altered cell.

A "host cell" is a cell which has been genetically altered, or is capable of being genetically altered, by administration of an exogenous polynucleotide.

5       The terms "cancerous cell" or "cancer cell", used either in the singular or plural form, refer to cells that have undergone a malignant transformation that makes them pathological to the host organism. Malignant transformation is a single- or multi-step process, which involves in part an alteration in the genetic makeup of the cell and/or the expression profile. Malignant transformation may occur either spontaneously, or via an event or combination of events such as drug or chemical  
10       treatment, radiation, fusion with other cells, viral infection, or activation or inactivation of particular genes. Malignant transformation may occur in vivo or in vitro, and can if necessary be experimentally induced.

A frequent feature of cancer cells is the tendency to grow in a manner that is uncontrollable by the host, but the pathology associated with a particular cancer cell may take another form, as  
15       outlined infra. Primary cancer cells (that is, cells obtained from near the site of malignant transformation) can be readily distinguished from non-cancerous cells by well-established techniques, particularly histological examination. The definition of a cancer cell, as used herein, includes not only a primary cancer cell, but any cell derived from a cancer cell ancestor. This includes metastasized cancer cells, and in vitro cultures and cell lines derived from cancer cells.

20       The "pathology" caused by a cancer cell within a host is anything that compromises the well-being or normal physiology of the host. This may involve (but is not limited to) abnormal or uncontrollable growth of the cell, metastasis, release of cytokines or other secretory products at an inappropriate level, manifestation of a function inappropriate for its physiological milieu, interference with the normal function of neighboring cells, aggravation or suppression of an inflammatory or  
25       immunological response, or the harboring of undesirable chemical agents or invasive organisms.

"Treatment" of an individual or a cell is any type of intervention in an attempt to alter the natural course of the individual or cell. For example, treatment of an individual may be undertaken to decrease or limit the pathology caused by a cancer cell harbored in the individual. Treatment includes (but is not limited to) administration of a composition, such as a pharmaceutical composition, and may  
30       be performed either prophylactically, or subsequent to the initiation of a pathologic event or contact with an etiologic agent. Effective amounts used in treatment are those which are sufficient to produce the desired effect, and may be given in single or divided doses.

A "control cell" is an alternative source of cells or an alternative cell line used in an experiment for comparison purposes. Where the purpose of the experiment is to establish a base line for gene  
35       copy number or expression level, it is generally preferable to use a control cell that is not a cancer cell.

The term "cancer gene" as used herein refers to any gene which is yielding transcription or translation products at a substantially altered level or in a substantially altered form in cancerous cells

compared with non-cancerous cells, and which may play a role in supporting the malignancy of the cell. It may be a normally quiescent gene that becomes activated (such as a dominant proto-oncogene), it may be a gene that becomes expressed at an abnormally high level (such as a growth factor receptor), it may be a gene that becomes mutated to produce a variant phenotype, or it may be a gene that becomes expressed at an abnormally low level (such as a tumor suppresser gene). The present invention is directed towards the discovery of genes in all these categories.

It is understood that a "clinical sample" encompasses a variety of sample types obtained from a subject and useful in an in vitro procedure, such as a diagnostic test. The definition encompasses solid tissue samples obtained as a surgical removal, a pathology specimen, or a biopsy specimen, tissue cultures or cells derived therefrom and the progeny thereof, and sections or smears prepared from any of these sources. Non-limiting examples are samples obtained from breast tissue, lymph nodes, and tumors. The definition also encompasses blood, spinal fluid, and other liquid sample of biologic origin, and may refer to either the cells or cell fragments suspended therein, or to the liquid medium and its solutes.

The term "relative amount" is used where a comparison is made between a test measurement and a control measurement. Thus, the relative amount of a reagent forming a complex in a reaction is the amount reacting with a test specimen, compared with the amount reacting with a control specimen. The control specimen may be run separately in the same assay, or it may be part of the same sample (for example, normal tissue surrounding a malignant area in a tissue section).

A "differential" result is generally obtained from an assay in which a comparison is made between the findings of two different assay samples, such as a cancerous cell line and a control cell line. Thus, for example, "differential expression" is observed when the level of expression of a particular gene is higher in one cell than another. "Differential display" refers to a display of a component, particularly RNA, from different cells to determine if there is a difference in the level of the component amongst different cells. Differential display of RNA is conducted, for example, by selective production and display of cDNA corresponding thereto. A method for performing differential display is provided in a later section.

A polynucleotide derived from or corresponding to CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, or CH14-2a16-1 is any of the following: the respective cDNA fragments, the corresponding messenger RNA, including splice variants and fragments thereof, both strands of the corresponding full-length cDNA and fragments thereof, and the corresponding gene. Isolated allelic variants of any of these forms are included. This invention embodies any polynucleotide corresponding to CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, or CH14-2a16-1 in an isolated form. It also embodies any such polynucleotide that has been cloned or transfected into a cell line.

When used in referring to the gene screening methods of this invention (such as those outlined in the last paragraph), "displaying cDNA" is any technique in which DNA copies of RNA (not restricted to mRNA) is rendered detectable in a quantitative or relatively quantitative fashion, in that DNA copies present in a relatively greater amount in a first sample compared with a second sample generates a relatively stronger or weaker signal compared with that of the second sample

due to the difference in copy number. Separate display of different cDNA in a preparation (particularly but not limited to cDNA of different size) allows comparison of levels of a particular cDNA between different samples. A preferred method of display is the differential display technique, and enhancements thereupon described in this disclosure and elsewhere.

5       The term "digested" DNA encompasses DNA (particularly chromosomal DNA) that has been fragmented by any suitable chemical or enzymatic means into fragments conveniently separable by standard techniques, particularly gel electrophoresis. Digestion with a restriction endonuclease specific for a particular nucleotide sequence is preferred.

10       "Hybridizing" in this context refers to contacting a first polynucleotide with a second polynucleotide under conditions that permit the formation of a multi-stranded polynucleotide duplex whenever one strand of the first polynucleotide has a sequence of sufficient complementarity to a sequence on the second polynucleotide. The duplex may be a long-lived one, such as when one DNA molecule is used as a labeled probe to detect another DNA molecule, that may optionally be bound to a nitrocellulose filter or present in a separating gel. The duplex may also be a shorter-  
15       lived one, such as when one DNA molecule is used to prime an amplification reaction of the other DNA molecule, and the amplified product is subsequently detected. The practitioner may alter the conditions of the reaction to alter the degree of complementarity required, as long as sequence specificity remains a determining factor in the reaction.

20       Unless explicitly indicated or otherwise required by the techniques used, the steps of a method of this invention may be performed in any order, or combined where desired and appropriate. In one example, in the method comprising steps a) through h) that is described above, it is entirely appropriate to conduct steps a) to c) of the method either before or after steps e) to g) of the method, as long as the cDNA ultimately selected fulfills the criteria of both steps d) and step h). In another example, screening against different digested DNA preparations, even if  
25       outlined separately, may optionally be done at the same time. All permutations of this kind are within the scope of the invention.

#### ***General methods***

30       The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, "Molecular Cloning: A Laboratory Manual", Second Edition (Sambrook, Fritsch & Maniatis, 1989), "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984), "Animal Cell Culture" (R.I. Freshney, ed., 1987);  
35       the series "Methods in Enzymology" (Academic Press, Inc.); "Handbook of Experimental Immunology" (D.M. Weir & C.C. Blackwell, Eds.), "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987), "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987); and "Current Protocols in Immunology" (J.E. Coligan et al., eds., 1991). All patents, patent applications,

articles and publications mentioned herein, both supra and infra, are hereby incorporated herein by reference.

*Features of the cancer gene screening method*

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The cancer gene screening methods of this invention may be brought to bear to discover novel genes associated with cancer. Exemplars of cancer-associated genes identified by this method are described below. The exemplars were identified using breast cancer cell lines and tissue, but the strategy can be applied to any cancer type of interest.

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A central feature of the cancer gene screening method of this invention is to look for both DNA duplication and RNA overabundance relating to the same gene. This feature is particularly powerful in the discovery of new and potentially important cancer genes. While amplicons occur frequently in cancer, the presently available techniques indicate only the broad chromosomal region involved in the duplication event, not the specific genes involved. The present invention provides a way of detecting genes that may be present in an amplicon from a functional basis. Because an early part of the method involves detecting RNA, the method avoids genes that may be duplicated in an amplicon but are quiescent (and therefore irrelevant) in the cancer cells. Furthermore, it recruits active genes from a duplicated region of the chromosome too small to be detectable by the techniques used to describe amplicons.

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Near the heart of this approach are several concepts. One is that genes encoding products implicated positively in the malignant process achieve elevated gene expression as a part of malignant transformation. In this context, "gene expression" refers to expression at the RNA transcription level. Most typically, the RNA is in turn be translated into a protein with a particular enzymatic, binding, or regulatory activity which increases after malignant transformation. In a less common example, the RNA may encode or participate as a ribozyme, antisense polynucleotide, or other functional nucleic acid molecule during malignancy. In a third example, RNA expression may be incidental but symptomatic of an important event in transformation.

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Another concept is that overexpression, if central to malignant transformation, may be achieved in different tumors by different mechanisms, and that at least one such possible mechanism is gene duplication. Accordingly, a substantial proportion of transformed cells will have an amplicon, or duplicated region of a chromosome, that includes within its compass the overexpressed gene. Other transformed cells may achieve RNA overabundance without gene duplication, such as by increasing the rate of transcription of the gene (e.g., by upregulation of the promoter region), by enhancing transcript promotion or transport, or by increasing mRNA survival.

35

Thus, the method entails screening at the RNA level, several cancer cell lines or tumors, and several normal cell lines or tissue samples at the same time. RNA are selected that show a consistent elevation amongst the cancer cells as compared with normal cells. Additional strategies may be employed in combination with the RNA screening to improve the success rate of the method. One such strategy is to use several cancer cell lines that are all known to have duplicated

genes in the same region of a particular chromosome. Thus, the RNA that emerge from the screen are more likely to represent a deliberate overexpression event, and the overexpressed gene is likely to be within the duplicated region. A supplemental strategy is to use freshly prepared tissue samples rather than cell lines as controls for base-line expression. This avoids selection of genes that may alter their expression level just as a result of tissue culturing. Another supplemental strategy is to conduct an additional level of screening, following identification of shared, overexpressed RNA. The selected RNA are used to screen DNA from suitable cancer cells and normal cells, to ensure that at least a proportion of the cells achieved the overexpression by way of gene duplication.

The strategy for detecting such genes comprises a number of innovations over those that have been used in previous work.

The first part of the method is based on a search for particular RNAs that are overabundant in cancer cells. A first innovation of the method is to compare RNA abundance between control cells and *several different cancer cells or cancer cell lines* of the desired type. The cDNA fragments that emerge in a greater amount in several different cancer lines, but not in control cells, are more likely to reflect genes that are important in disease progression, rather than those that have undergone secondary or coincidental activation. It is particularly preferred to use cancer cells that are known to share a common duplicated chromosomal region.

A second innovation of this method is to supply as control, not RNA from a cell line or culture, but from *fresh tissue samples* of non-malignant origin. There are two reasons for this. First, the tissue will provide the spectrum of expression that is typical to the normal cell phenotype, rather than individual differences that may become more prominent in culture. This establishes a more reliable baseline for normal expression levels. More importantly, the tissue will be devoid of the effects that in vitro culturing may have in altering or selecting particular phenotypes. For example, proto-oncogenes or growth factors may become up-regulated in culture. When cultured cells are used as the control for differential display, these up-regulated genes would be missed.

A third innovation of this method is to undertake a subselection for cDNA corresponding to genes that achieve their RNA overabundance in a substantial proportion of cancer cells by gene duplication. To accomplish this, appropriate cDNA corresponding to overabundant RNA identified in the foregoing steps are used to probe digests of cellular DNA from a panel of different cancer cells, and from normal genomic DNA. cDNA that shows evidence of higher copy numbers in a proportion of the panel are selected for further characterization. An additional advantage of this step is that cDNA corresponding to mitochondrial genes can rapidly be screened away by including a mitochondrial DNA digest as an additional sample for testing the probe. This eliminates most of the false-positive cDNA, which otherwise make up a majority of the cDNA identified.

Thus, the identification of genes yielding products that are present at abnormal levels is accomplished by a method comprised of the following steps.

To identify particular RNA that is overabundant in cancer cells, RNA is prepared from both cancerous and control cells by standard techniques. Cancer-associated genes may affect cellular

metabolism by any one of a number of mechanisms. For example, they may encode ribozymes, anti-sense polynucleotides, DNA-binding polynucleotides, altered ribosomal RNA, and the like. The gene screening methods of this invention may employ a comparison of RNA abundance levels at the total RNA level, not strictly limited to mRNA. However, the vast majority of cancer-associated genes are predicted to encode a protein gene whose up-regulation is closely linked to the metabolic process. For example, the four exemplary breast cancer genes described elsewhere in this application all comprise an open reading frame. Accordingly, a focus on mRNA enriches the selectable pool for candidate cancer-associated genes. Focus towards mRNA can be conducted at any step in the method. It is particularly convenient to use a display method that displays cDNA copied only from mRNA. In this case, whole RNA may be prepared and analyzed from cancer and control cell populations without separating out mRNA.

In terms of the cancer cells used as an RNA source, it is particularly advantageous to use a plurality of cancer cells known to contain a duplicated gene or chromosomal segment in the same region of the chromosome. The duplicated segment need not be the same size in all the cells, nor is it necessary that the number of duplications be the same, so long as there is at least some part of the duplicated segment that is shared amongst all the cancer cells used in the screen. Thus, a minimum of two, and preferably at least three cancer cells are used that are sufficiently characterized to identify a shared duplicated region, and can be used as a source of RNA for the screening test. In contrast, the control cell population will not comprise chromosomal duplications.

Assuming the duplication to be related to the malignancy of the cancer cells, RNA transcribed from the duplicated region is expected to be overabundant compared with that of the control cell. Accordingly, a highly effective strategy is to identify overabundant RNA that is present in *all* (or *at least several*) of the cancer cell preparations, but none of the control preparations. By using cancer cells that share a duplicated chromosomal region, the RNA comparison will be strongly biased in favor of RNA overabundance transcribed from the shared duplicated region. Since the shared region is optimally only a small segment of a single chromosome, expression differences arising from elsewhere in the genome in one cancer cell or another will not be selected. We have found that this is highly effective in eliminating: a) RNA abundance differences resulting from normal metabolic variations between cells; and/or b) RNA abundance differences related to cancer cell malignancy, but occurring secondarily to malignant transformation. This is important, because it considerably minimizes the chief deficiency in the use of RNA comparison methods, particularly differential display, for the screening of potential cancer genes: namely, the onerous number of false-positives that such techniques generate.

Shared duplicated regions in cancer cells may be identified by a relevant analytical technique, or by reference to such analysis already conducted and published. One approach that has been highly effective in mapping approximate sub-chromosomal locations of duplicated segments is comparative genomic hybridization (CGH). This technique involves extracting, amplifying and labeling DNA from the subject cell; hybridizing to reference metaphase chromosomes treated to remove repetitive sequences; and observing the position of the hybridized



DNA on the chromosomes (WO 93/18186; Gray et al.). The greater the signal intensity at a given position, the greater the copy number of the sequences in the subject cell. Thus, regions showing elevated staining correspond to genes duplicated in the cancer cells, while regions showing diminished staining correspond to genes deleted in the cancer cells. Related techniques which a practitioner in the art will be well aware are methods for preparing and using repeat sequence chromosome-specific nucleic acid probes (US 5,427,932; Weier et al.), methods for staining target chromosomal DNA using labeled nucleic acid fragments in conjunction with blocking fragments complementary to repetitive DNA segments (US 5,447,841; Gray et al.), and methods for detecting amplified or deleted chromosomal regions using a mapped library of labeled polynucleotide probes (US 5,472,842; Stokke et al.). If desired, multiple fluorochromes can be used as labeling agents with CGH and related techniques, to provide a three-color visualization of deleted, normal, and duplicated chromosome abnormalities (Lucas et al.).

The choice of a particular chromosomal mapping approach is irrelevant, especially once knowledge of the duplicated region is known. If the location of the chromosome duplication is already established for a cell line to be used in RNA comparison during the course of the present invention, then it is unnecessary to conduct a mapping technique *de novo*. For example, established cancer cell lines exist for which mapping data is already available in the public domain. Provided in the reference section of this application is a list of over 40 articles in which the locations of duplicated regions in particular cancer cells are described. In the context of the present invention, a plurality of cancer cells is chosen for the screening panel based on such data, so that they share a duplicated chromosomal region. The chromosomal location of a suspected duplication may be confirmed by hybridization analysis, if desired, using a probe specific for the location.

The cancer cells used for RNA comparison are also generally (but not necessarily) derived from the same type of cancer or the same tissue. Using cells derived from the same type of cancer increases the probability that the gene ultimately identified will be common in that type of cancer, and suitable as a type-specific diagnostic marker. Using cells derived from different types of cancer is in effect a search for cancer-related genes that are less tissue specific and more related to the malignant process in general. Both types of genes are of interest for both diagnostic and therapeutic purposes. In one illustration highlighted in Example 1, RNA was screened from the three breast cancer cell lines BT474, SKBR3, and MCF7, which have been determined by CGH or Southern analysis to share a duplicated genetic regions in chromosomes 1, 8, 14, 17, and 20. When the RNA from these cells was displayed, a number of RNA were found to be overabundant in the cancer cells, but not controls (Figure 1). Three RNA overabundant in all three cancer cell lines corresponded to cancer-associated genes located on chromosomes 1, 8, and 14 that are listed in Table 1. The chromosome 13 gene (CH13-2a12-1) was overexpressed in 2 of the 3 cell lines; namely BT474 and SKBR3. Southern analysis subsequently established that the chromosome 13 gene was duplicated in the same two cell lines (Example 6, Table 5).

Selection of the source or sources of control cell RNA is also a matter of some refinement. The control RNA can be derived from in vitro cultures of non-malignant cells, or established cell lines derived from a non-malignant source. However, it is preferable for the control RNA to be obtained directly from normal human tissue of the same type as the cancer cells. This is because most normal cells do not proliferate indefinitely; hence adaptation of a cell into a cell line involves a degree of transformation. The transforming event may, in turn, be shared with that of certain cancer cells, at least at the level of RNA abundance. Hence, comparison of the RNA levels in cancer cells with so-called control cell lines may lead the practitioner to miss genes that are related to malignancy. For convenience, control cells may be maintained in culture for a brief period before the experiment, and even stimulated; however, multiple rounds of cell division are to be avoided if possible. Use of both stimulated and unstimulated cells as controls may help provide RNA patterns corresponding to the normal range of abundance within various metabolic events of the cell cycle. In one illustration highlighted in Example 1, RNA was screened using both proliferating and non-proliferating cells. As stated, the screening of breast cancer RNA is preferably conducted using uncultured normal mammary epithelial cells (termed "organoids") as sources of control RNA. These cells may be obtained from surgical samples resected from healthy breast tissue.

The RNA is preserved until use in the comparison experiment in such a way to minimize fragmentation. To facilitate confirmation experiments, it is useful to use RNA of a reproducible character. For this reason, it is convenient to use RNA that has been obtained from stable cancerous cell lines and/or ready tissue sources, although reproducibility can also be provided by preparing enough RNA so that it can be preserved in aliquots.

For displaying relative overabundance of RNA in the cancer cells, compared with the control cells, many standard techniques are suitable. These would include any form of subtractive hybridization or comparative analysis. Preferred are techniques in which more than two RNA sources are compared at the same time, such as various types of arbitrarily primed PCR fingerprinting techniques (Welsh et al., Yoshikawa et al.). Particularly preferred are differential mRNA display methods and variations thereof, in which the samples are run in neighboring lanes in a separating gel. These techniques are focused towards mRNA by using primers that are specific for the poly-A tail characteristic of mRNA (Liang et al., 1992a; U.S. Patent 5,262,311).

Because many thousands of genes are expressed in the cells of higher organisms at any one time, it is preferable to improve the legibility of the display by surveying only a subset of the RNA at a time. Methods for accomplishing this are known in the art. A preferred method is by using selective primers that initiate PCR replication for a subset of the RNA. Thus, the RNA is first reverse transcribed by standard techniques. Short primers are used for the selection, preferably chosen such that alternative primers used in a series of like assays can complete a comprehensive survey of the mRNA.

In a preferred example, primers can be used for the 3' region of the mRNAs which have an oligo-dT sequence, followed by two other nucleotides (TiNM, where  $i \approx 11$ ,  $N \in \{A, C, G\}$ , and  $M \in$

{A,C,G,T}). Thus, 12 possible primers are required to complete the survey. A random or arbitrary primer of minimal length can then be used for replication towards what corresponds in the sequence to the 5' region of the mRNA. The optimal length for the random primer is about 10 nucleotides. The product of the PCR reaction is labeled with a radioisotope, such as <sup>35</sup>S. The labeled cDNA is then separated by molecular weight, such as on a polyacrylamide sequencing gel.

If desired, variations on the differential display technique may be employed. For example, one-base oligo-dT primers may be used (Liang et al., 1993 & 1994), although this is generally less preferred because the display pattern is correspondingly more complex. Selection of primers may be optimized mathematically depending on the number of RNA species in a tissue of interest (Bauer et al.). The method may be adapted for non-denaturing gels, and for use with automatic DNA sequencers (Bauer et al.). Alternative radioisotopes (Trentmann et al.) or fluorochromes (Sun et al.) may be used for labeling the differential display. Differential display may optionally be combined with a ribonuclease protection assay (Yeatman et al.). PCR primers may optionally incorporate a restriction site to facilitate cloning (Linskens et al., Ayala et al.). Using *Taq* polymerase from multiple manufacturers can increase the amount of variation under otherwise identical conditions (Haag et al.). Nested PCR primers may be used in differential display to decrease background created by oligo-dT primers (WO 95/33760). Other variants of the differential display technique are known in the art and described *inter alia* in the references cited in this disclosure. The use of such modifications are within the scope of the present invention, but are not required, as evidenced by the examples described below.

Based on the comparison of relative abundance of RNA, particular RNAs are chosen which are present as a higher proportion of the RNA in cancerous cells, compared with control cells. When using the differential display method, the cDNA corresponding to overabundant RNA will produce a band with greater proportional intensity amongst neighboring cDNA bands, compared with the proportional intensity in the control lanes. Desired cDNAs can be recovered most directly by cutting the spot in the gel corresponding to the band, and recovering the DNAs therefrom. Recovered cDNA can be replicated again for further use by any technique or combination of techniques known in the art, including PCR and cloning into a suitable carrier.

An optional but highly beneficial additional screening step, typically performed subsequently to an RNA comparison as described above, is aimed at identifying genes that are duplicated in a substantial proportion of cancers. This is conducted by using cDNA such as selected from differential display to probe digests of chromosomal DNA obtained from two or more cancerous cells, such as cancer cell lines. Chromosomal DNA from non-cancerous cells that essentially reflects the germ line in terms of gene copy number is used for the control. A preferred source of control DNA in experiments for human cancer genes is placental DNA, which is readily obtainable. The DNA samples are cleaved at sequence-specific sites along the chromosome, most usually with a suitable restriction enzyme into fragments of appropriate size. The DNA can be blotted directly onto a suitable medium, or separated on an agarose gel before blotting. The latter method is preferred, because it enables a comparison of the hybridizing chromosomal restriction

fragment to determine whether the probe is binding to the same fragment in all samples. The amount of probe binding to DNA digests from each of the cancer cells is compared with the amount binding to control DNA.

Because the comparison is quantitative, it is preferable to standardize the measurement internally. One method is to administer a second probe to the same blot, probing for a second chromosomal gene unlikely to be duplicated in the cancer cells. This method is preferred, because it standardizes not only for differences in the amount of DNA provided, but also for differences in the amount transferred during blotting. This can be accomplished by using alternative labels for the two probes, or by stripping the first probe with a suitable eluant before administering the second.

To eliminate cDNA for mitochondrial genes, it is preferable to include in a parallel analysis a mitochondrial DNA preparation digested with the same restriction enzyme. Any cDNA probe that hybridizes to the appropriate mitochondrial restriction fragments can be suspected of corresponding to a mitochondrial gene.

In the initial replication of the RNA, the random primer may bind at any location along the RNA sequence. Thus, the copied and replicated segment may be a fragment of the full-length RNA. Longer cDNA corresponding to a greater portion of the sequence can be obtained, if desired, by several techniques known to practitioners of ordinary skill. These include using the cDNA fragment to isolate the corresponding RNA, or to isolate complementary DNA from a cDNA library of the same species. Preferably, the library is derived from the same tissue source, and more preferably from a cancer cell line of the same type. For example, for cDNA corresponding to human breast cancer genes, a preferred library is derived from breast cancer cell line BT474, constructed in lambda GT10.

Sequences of the cDNA can be determined by standard techniques, or by submitting the sample to commercial sequencing services. The chromosomal locations of the genes can be determined by any one of several methods known in the art, such as in situ hybridization using chromosomal smears, or panels of somatic cell hybrids of known chromosomal composition.

The cDNA obtained through the selection process outlined can then be tested against a larger panel of cancer cell lines and/or fresh tumor cells to determine what proportion of the cells have duplicated the gene. This can be accomplished by using the cDNA as a probe for chromosomal DNA digests, as described earlier. As illustrated in the Example section, a preferred method for conducting this determination is Southern analysis.

The cDNA can also be used to determine what proportion of the cells have RNA overabundance. This can be accomplished by standard techniques, such as slot blots or blots of agarose gels, using whole RNA or messenger RNA from each of the cells in the panel. The blots are then probed with the cDNA using standard techniques. It is preferable to provide an internal loading and blotting control for this analysis. A preferred method is to re-probe the same blot for transcripts of a gene likely to be present in about the same level in all cells of the same type, such as the gene for a cytoskeletal protein. Thus, a preferred second probe is the cDNA for beta-actin.

Using a novel cDNA found by this selection procedure, it is anticipated that essentially all cancer cells showing gene duplication will also show RNA overabundance, but that some will show RNA overabundance without gene duplication.

The practitioner will readily appreciate that the strategies for identifying genes that are duplicated and/or associated with RNA overabundance may be reversed appropriately to screen for genes that are deleted and/or associated with RNA underabundance. The principles are essentially the same. Genes that are frequently down-regulated in cancer (such as tumor suppresser genes) may be down-regulated by different mechanisms in different cells, and a gene with this behavior is more likely to be central to malignant transformation or persistence of the malignant state.

To screen for such down-regulated genes according to the present invention, RNA is prepared from a plurality of tumors or cancer cell lines and the abundance is compared with RNA preparation from control cells. Again, it is highly preferable to use cancer cells that share a deleted gene in the same chromosomal region, in order to focus any differences at the RNA level towards particular alterations in cancer cells and away from normal variations or coincidental changes. The CGH technique may be used to identify deletions in previously uncharacterized cancer cells. As before, cancer cells may be chosen on the basis of previous knowledge of deleted regions; there is no need to conduct methods such as CGH on previously characterized lines. cDNA from the RNA of cancer cells is displayed (preferably by differential display) alongside cDNA copied from (preferably uncultured) control cells, and cDNA is selected that appears to be underrepresented in at least two (preferably more) of the cancer cells compared with the control cells. cDNA thus selected may optionally be further screened against digested DNA preparations, to confirm that the RNA underabundance observed in the cancer cell populations is attributable in at least a proportion of the cells to an actual gene deletion.

As before, the cDNA may be used for sequencing or rescuing additional polynucleotides, in this case not from the cancer cells but from cells containing or expressing the gene at normal levels. Pharmaceuticals based on deleted genes or those associated with underexpressed RNA are typically oriented at restoring or upregulating the gene, or a functional equivalent of the encoded gene product.

#### ***The identification of four exemplary cancer associated genes***

To identify particular RNA that is overabundant in cancer cells, RNA has been compared between breast cancer cells and control cells. The amount of total cellular RNA was compared using a modified differential display method. Primers were used for the 3' region of the mRNAs which have an oligo-dT sequence, followed by two other nucleotides as described in the previous section. Random or arbitrary primers of about 10 nucleotides were used for replication towards what corresponds in the sequence to the 5' region of the mRNA. The labeled amplification product was then separated by molecular weight on a polyacrylamide sequencing gel.

Particular mRNAs were chosen that were present in a higher proportion of the RNA in cancerous cells, compared with control cells, according to the proportional intensity amongst neighboring cDNA bands. The cDNA was recovered directly from the gel and amplified to provide a probe for screening. Candidate polynucleotides were screened by a number of criteria, including both Northern and Southern analysis to determine if the corresponding genes were duplicated or responsible for to RNA overabundance in breast cancer cells. Sequence data of the polynucleotides was obtained and compared with sequences in GenBank. Novel polynucleotides with the desired expression patterns were used to probe for longer cDNA inserts in a  $\lambda$ gt10 library constructed from the breast cancer cell line BT474, which were then sequenced.

Further description of the actual experimental events that occurred during identification of the four exemplary genes, and sequence data for CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1 are provided in the Example section.

#### *Preparation of polynucleotides, polypeptides and antibodies*

Polynucleotides based on the cDNA of CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, CH14-2a16-1, can be rescued from cloned plasmids and phage provided as part of this invention. They may also be obtained from breast cancer cell libraries or mRNA preparations, or from normal human tissues such as placenta, by judicious use of primers or probes based on the sequence data provided herein. Alternatively, the sequence data provided herein can be used in chemical synthesis to produce a polynucleotide with an identical sequence, or that incorporates occasional variations.

Polypeptides encoded by the corresponding mRNA can be prepared by several different methods, all of which will be known to a practitioner of ordinary skill. For example, the appropriate strand of the full-length cDNA can be operably linked to a suitable promoter, and transfected into a suitable host cell. The host cell is then cultured under conditions that allow transcription and translation to occur, and the polypeptide is subsequently recovered. Another convenient method is to determine the polynucleotide sequence of the cDNA, and predict the polypeptide sequence according to the genetic code. A polypeptide can then be prepared directly, for example, by chemical synthesis, either identical to the predicted sequence, or incorporating occasional variations.

Antibodies against polypeptides of this invention may be prepared by any method known in the art. For stimulating antibody production in an animal, it is often preferable to enhance the immunogenicity of a polypeptide by such techniques as polymerization with glutaraldehyde, or combining with an adjuvant, such as Freund's adjuvant. The immunogen is injected into a suitable experimental animal: preferably a rodent for the preparation of monoclonal antibodies; preferably a larger animal such as a rabbit or sheep for preparation of polyclonal antibodies. It is preferable to provide a second or booster injection after about 4 weeks, and begin harvesting the antibody source no less than about 1 week later.

Sera harvested from the immunized animals provide a source of polyclonal antibodies. Detailed procedures for purifying specific antibody activity from a source material are known within the

art. Unwanted activity cross-reacting with other antigens, if present, can be removed, for example, by running the preparation over adsorbants made of those antigens attached to a solid phase, and collecting the unbound fraction. If desired, the specific antibody activity can be further purified by such techniques as protein A chromatography, ammonium sulfate precipitation, ion exchange  
5 chromatography, high-performance liquid chromatography and immunoaffinity chromatography on a column of the immunizing polypeptide coupled to a solid support.

Alternatively, immune cells such as splenocytes can be recovered from the immunized animals and used to prepare a monoclonal antibody-producing cell line. See, for example, Harrow & Lane (1988), U.S. Patent Nos. 4,491,632 (J.R. Wands et al.), U.S. 4,472,500 (C. Milstein et al.), and  
10 U.S. 4,444,887 (M.K. Hoffman et al.)

Briefly, an antibody-producing line can be produced inter alia by cell fusion, or by transfecting antibody-producing cells with Epstein Barr Virus, or transforming with oncogenic DNA. The treated cells are cloned and cultured, and clones are selected that produce antibody of the desired specificity. Specificity testing can be performed on culture supernatants by a number of techniques, such as  
15 using the immunizing polypeptide as the detecting reagent in a standard immunoassay, or using cells expressing the polypeptide in immunohistochemistry. A supply of monoclonal antibody from the selected clones can be purified from a large volume of tissue culture supernatant, or from the ascites fluid of suitably prepared host animals injected with the clone.

Effective variations of this method include those in which the immunization with the  
20 polypeptide is performed on isolated cells. Antibody fragments and other derivatives can be prepared by methods of standard protein chemistry, such as subjecting the antibody to cleavage with a proteolytic enzyme. Genetically engineered variants of the antibody can be produced by obtaining a polynucleotide encoding the antibody, and applying the general methods of molecular biology to introduce mutations and translate the variant.

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#### *Use in diagnosis*

Novel cDNA sequences corresponding to genes associated with cancer are potentially useful as diagnostic aids. Similarly, polypeptides encoded by such genes, and antibodies specific for these  
30 polypeptides, are also potentially useful as diagnostic aids.

More specifically, gene duplication or overabundance of RNA in particular cells can help identify those cells as being cancerous, and thereby play a part in the initial diagnosis. Increased levels of RNA corresponding to CH1-9a11-2, CH8-2a13-12, CH13-2a12-1, and CH14-2a16-1 are present in a substantial proportion of breast cancer cell lines and primary breast tumors. In addition,  
35 preliminary Northern analysis using probes for CH8-2a13-12, CH13-2a12-1, and CH14-2a16-1 indicates that these genes may be duplicated or be associated with RNA overabundance in certain cell lines derived from cancers other than breast cancer, including colon cancer, lung cancer, prostate cancer, glioma, and ovarian cancer.

For patients already diagnosed with cancer, gene duplication or overabundance of RNA can assist with clinical management and prognosis. For example, overabundance of RNA may be a useful predictor of disease survival, metastasis, susceptibility to various regimens of standard chemotherapy, the stage of the cancer, or its aggressiveness. See generally the article by Blast, U.S. Patent No. 4,968,603 (Slamon et al.) and PCT Application WO 94/00601 (Levine et al.). All of these determinations are important in helping the clinician choose between the available treatment options.

A particularly important diagnostic application contemplated in this invention is the identification of patients suitable for gene-specific therapy, as outlined in the following section. For example, treatment directed against a particular gene or gene product is appropriate in cancers where the gene is duplicated or there is RNA overabundance. Given a particular pharmaceutical that is directed at a particular gene, a diagnostic test specific for the same gene is important in selecting patients likely to benefit from the pharmaceutical. Given a selection of such pharmaceuticals specific for different genes, diagnostic tests for each gene are important in selecting which pharmaceutical is likely to benefit a particular patient.

The polynucleotide, polypeptide, and antibodies embodied in this invention provide specific reagents that can be used in standard diagnostic procedures. The actual procedures for conducting diagnostic tests are extensively known in the art, and are routine for a practitioner of ordinary skill. See, for example, U.S. Patent No. 4,968,603 (Slamon et al.), and PCT Applications WO 94/00601 (Levine et al.) and WO 94/17414 (K. Keyomarsi et al.). What follows is a brief non-limiting survey of some of the known procedures that can be applied.

Generally, to perform a diagnostic method of this invention, one of the compositions of this invention is provided as a reagent to detect a target in a clinical sample with which it reacts. Thus, the polynucleotide of this invention can be used as a reagent to detect a DNA or RNA target, such as might be present in a cell with duplication or RNA overabundance of the corresponding gene. The polypeptide can be used as a reagent to detect a target for which it has a specific binding site, such as an antibody molecule or (if the polypeptide is a receptor) the corresponding ligand. The antibody can be used as a reagent to detect a target it specifically recognizes, such as the polypeptide used as an immunogen to raise it.

The target is supplied by obtaining a suitable tissue sample from an individual for whom the diagnostic parameter is to be measured. Relevant test samples are those obtained from individuals suspected of containing cancerous cells, particularly breast cancer cells. Many types of samples are suitable for this purpose, including those that are obtained near the suspected tumor site by biopsy or surgical dissection, in vitro cultures of cells derived therefrom, blood, and blood components. If desired, the target may be partially purified from the sample or amplified before the assay is conducted. The reaction is performed by contacting the reagent with the sample under conditions that will allow a complex to form between the reagent and the target. The reaction may be performed in solution, or on a solid tissue sample, for example, using histology sections. The formation of the complex is detected by a number of techniques known in the art. For example, the reagent may be supplied with a label and unreacted reagent may be removed from the complex; the amount of



remaining label thereby indicating the amount of complex formed. Further details and alternatives for complex detection are provided in the descriptions that follow.

To determine whether the amount of complex formed is representative of cancerous or non-cancerous cells, the assay result is compared with a similar assay conducted on a control sample. It is generally preferable to use a control sample which is from a non-cancerous source, and otherwise similar in composition to the clinical sample being tested. However, any control sample may be suitable provided the relative amount of target in the control is known or can be used for comparative purposes. Where the assay is being conducted on tissue sections, suitable control cells with normal histopathology may surround the cancerous cells being tested. It is often preferable to conduct the assay on the test sample and the control sample simultaneously. However, if the amount of complex formed is quantifiable and sufficiently consistent, it is acceptable to assay the test sample and control sample on different days or in different laboratories.

A polynucleotide embodied in this invention can be used as a reagent for determining gene duplication or RNA overabundance that may be present in a clinical sample. The binding of the reagent polynucleotide to a target in a clinical sample generally relies in part on a hybridization reaction between a region of the polynucleotide reagent, and the DNA or RNA in a sample being tested.

If desired, the nucleic acid may be extracted from the sample, and may also be partially purified. To measure gene duplication, the preparation is preferably enriched for chromosomal DNA; to measure RNA overabundance, the preparation is preferably enriched for RNA. The target polynucleotide can be optionally subjected to any combination of additional treatments, including digestion with restriction endonucleases, size separation, for example by electrophoresis in agarose or polyacrylamide, and affixed to a reaction matrix, such as a blotting material.

Hybridization is allowed to occur by mixing the reagent polynucleotide with a sample suspected of containing a target polynucleotide under appropriate reaction conditions. This may be followed by washing or separation to remove unreacted reagent. Generally, both the target polynucleotide and the reagent must be at least partly equilibrated into the single-stranded form in order for complementary sequences to hybridize efficiently. Thus, it may be useful (particularly in tests for DNA) to prepare the sample by standard denaturation techniques known in the art.

The minimum complementarity between the reagent sequence and the target sequence for a complex to form depends on the conditions under which the complex-forming reaction is allowed to occur. Such conditions include temperature, ionic strength, time of incubation, the presence of additional solutes in the reaction mixture such as formamide, and washing procedure. Higher stringency conditions are those under which higher minimum complementarity is required for stable hybridization to occur. It is generally preferable in diagnostic applications to increase the specificity of the reaction, minimizing cross-reactivity of the reagent polynucleotide alternative undesired hybridization sites in the sample. Thus, it is preferable to conduct the reaction under conditions of high stringency: for example, in the presence of high temperature, low salt, formamide, a combination of these, or followed by a low-salt wash.

In order to detect the complexes formed between the reagent and the target, the reagent is generally provided with a label. Some of the labels often used in this type of assay include radioisotopes such as  $^{32}\text{P}$  and  $^{33}\text{P}$ , chemiluminescent or fluorescent reagents such as fluorescein, and enzymes such as alkaline phosphatase that are capable of producing a colored solute or precipitant.

5 The label may be intrinsic to the reagent, it may be attached by direct chemical linkage, or it may be connected through a series of intermediate reactive molecules, such as a biotin-avidin complex, or a series of inter-reactive polynucleotides. The label may be added to the reagent before hybridization with the target polynucleotide, or afterwards.

To improve the sensitivity of the assay, it is often desirable to increase the signal ensuing from hybridization. This can be accomplished by replicating either the target polynucleotide or the reagent polynucleotide, such as by a polymerase chain reaction. Alternatively, a combination of serially hybridizing polynucleotides or branched polynucleotides can be used in such a way that multiple label components become incorporated into each complex. See U.S. Patent No. 5,124,246 (Urdea et al.).

15 An antibody embodied in this invention can also be used as a reagent in cancer diagnosis, or for determining gene duplication or RNA overabundance that may be present in a clinical sample. This relies on the fact that overabundance of RNA in affected cells is often associated with increased production of the corresponding polypeptide. Several of the genes up-regulated in cancer cells encode for cell surface receptors. For example, *erbB-2*, *c-myc* and epidermal growth factor.

20 Alternatively, the RNA may encode a protein kept inside the cell, or it may encode a protein secreted by the cell into the surrounding milieu.

Any such protein product can be detected in solid tissue samples and cultured cells by immunohistological techniques that will be obvious to a practitioner of ordinary skill. Generally, the tissue is preserved by a combination of techniques which may include cooling, exchanging into different solvents, fixing with agents such as paraformaldehyde, or embedding in a commercially available medium such as paraffin or OCT. A section of the sample is suitably prepared and overlaid with a primary antibody specific for the protein.

The primary antibody may be provided directly with a suitable label. More frequently, the primary antibody is detected using one of a number of developing reagents which are easily produced or available commercially. Typically, these developing reagents are anti-immunoglobulin or protein A, and they typically bear labels which include, but are not limited to: fluorescent markers such as fluorescein, enzymes such as peroxidase that are capable of precipitating a suitable chemical compound, electron dense markers such as colloidal gold, or radioisotopes such as  $^{125}\text{I}$ . The section is then visualized using an appropriate microscopic technique, and the level of labeling is compared between the suspected cancer cell and a control cell, such as cells surrounding the tumor area or those taken from an alternative site.

The amount of protein corresponding to the cancer-associated gene may be detected in a standard quantitative immunoassay. If the protein is secreted or shed from the cell in any appreciable amount, it may be detectable in plasma or serum samples. Alternatively, the target protein may be

solubilized or extracted from a solid tissue sample. Before quantitating, the protein may optionally be affixed to a solid phase, such as by a blot technique or using a capture antibody.

A number of immunoassay methods are established in the art for performing the quantitation. For example, the protein may be mixed with a pre-determined non-limiting amount of the reagent antibody specific for the protein. The reagent antibody may contain a directly attached label, such as an enzyme or a radioisotope, or a second labeled reagent may be added, such as anti-immunoglobulin or protein A. For a solid-phase assay, unreacted reagents are removed by washing. For a liquid-phase assay, unreacted reagents are removed by some other separation technique, such as filtration or chromatography. The amount of label captured in the complex is positively related to the amount of target protein present in the test sample. A variation of this technique is a competitive assay, in which the target protein competes with a labeled analog for binding sites on the specific antibody. In this case, the amount of label captured is negatively related to the amount of target protein present in a test sample. Results obtained using any such assay on a sample from a suspected cancer-bearing source are compared with those from a non-cancerous source.

A polypeptide embodied in this invention can also be used as a reagent in cancer diagnosis, or for determining gene duplication or RNA overabundance that may be present in a clinical sample. Overabundance of RNA in affected cells may result in the corresponding polypeptide being produced by the cells in an abnormal amount. On occasion, overabundance of RNA may occur concurrently with expression of the polypeptide in an unusual form. This in turn may result in stimulation of the immune response of the host to produce its own antibody molecules that are specific for the polypeptide. Thus, a number of human hybridomas have been raised from cancer patients that produce antibodies against their own tumor antigens.

To use the polypeptide in the detection of such antibodies in a subject suspected of having cancer, an immunoassay is conducted. Suitable methods are generally the same as the immunoassays outlined in the preceding paragraphs, except that the polypeptide is provided as a reagent, and the antibody is the target in the clinical sample which is to be quantified. For example, human IgG antibody molecules present in a serum sample may be captured with solid-phase protein A, and then overlaid with the labeled polypeptide reagent. The amount of antibody would then be proportional to the label attached to the solid phase. Alternatively, cells or tissue sections expressing the polypeptide may be overlaid first with the test sample containing the antibody, and then with a detecting reagent such as labeled anti-immunoglobulin. The amount of antibody would then be proportional to the label attached to the cells. The amount of antibody detected in the sample from a suspected cancerous source would be compared with the amount detected in a control sample.

These diagnostic procedures may be performed by diagnostic laboratories, experimental laboratories, practitioners, or private individuals. This invention provides diagnostic kits which can be used in these settings. The presence of cancer cells in the individual may be manifest in a clinical sample obtained from that individual as an alteration in the DNA, RNA, protein, or antibodies contained in the sample. An alteration in one of these components resulting from the presence of

cancer may take the form of an increase or decrease of the level of the component, or an alteration in the form of the component, compared with that in a sample from a healthy individual. The clinical sample is optionally pre-treated for enrichment of the target being tested for. The user then applies a reagent contained in the kit in order to detect the changed level or alteration in the diagnostic component.

Each kit necessarily comprises the reagent which renders the procedure specific: a reagent polynucleotide, used for detecting target DNA or RNA; a reagent antibody, used for detecting target protein; or a reagent polypeptide, used for detecting target antibody that may be present in a sample to be analyzed. The reagent is supplied in a solid form or liquid buffer that is suitable for inventory storage, and later for exchange or addition into the reaction medium when the test is performed. Suitable packaging is provided. The kit may optionally provide additional components that are useful in the procedure. These optional components include buffers, capture reagents, developing reagents, labels, reacting surfaces, means for detection, control samples, instructions, and interpretive information.

#### *Use in pharmaceutical development*

Embodied in this invention are modes of treating subjects bearing cancer cells that have overabundance of the particular RNA described. The strategy used to obtain the cDNAs provided in this invention was deliberately focused on genes that achieve RNA overabundance by gene duplication in some cells, and by alternative mechanisms in other cells. These alternative mechanisms may include, for example, translocation or enhancement of transcription enhancing elements near the coding region of the gene, deletion of repressor binding sites, or altered production of gene regulators. Such mechanisms would result in more RNA being transcribed from the same gene. Alternatively, the same amount of RNA may be transcribed, but may persist longer in the cell, resulting in greater abundance. This could occur, for example, by reduction in the level of ribozymes or protein enzymes that degrade RNA, or in the modification of the RNA to render it more resistant to such enzymes or spontaneous degradation.

Thus, different cells make use of at least two different mechanisms to achieve a single result: the overabundance of a particular RNA. This suggests that RNA overabundance of these genes is central to the cancer process in the affected cells. Interfering with the specific gene or gene product would consequently modify the cancer process. It is an objective of this invention to provide pharmaceutical compositions that enable therapy of this kind.

One way this invention achieves this objective is through screening candidate drugs. The general screening strategy is to apply the candidate to a manifestation of a gene associated with cancer, and then determine whether the effect is beneficial and specific. For example, a composition that interferes with a polynucleotide or polypeptide corresponding any of the novel cancer-associated genes described herein has the potential to block the associated pathology when administered to a tumor of the appropriate phenotype. It is not necessary that the mechanism of interference be known;

only that the interference be preferential for cancerous cells (or cells near the cancer site) but not other cells.

5 A preferred method of screening is to provide cells in which a polynucleotide related to a cancer gene has been transfected. See, for example, PCT application WO 93/08701. A practitioner of ordinary skill will be well acquainted with techniques for transfecting eukaryotic cells, including the preparation of a suitable vector, such as a viral vector; conveying the vector into the cell, such as by electroporation; and selecting cells that have been transformed, such as by using a reporter or drug sensitivity element.

10 A cell line is chosen which has a phenotype desirable in testing, and which can be maintained well in culture. The cell line is transfected with a polynucleotide corresponding to one of the cancer-associated genes identified herein. Transfection is performed such that the polynucleotide is operably linked to a genetic controlling element that permits the correct strand of the polynucleotide to be transcribed within the cell. Successful transfection can be determined by the increased abundance of the RNA compared with an untransfected cell. It is not necessary that the cell previously be devoid of the RNA, only that the transfection result in a substantial increase in the level observed. RNA abundance in the cell is measured using the same polynucleotide, according to the hybridization assays outlined earlier.

15 Drug screening is performed by adding each candidate to a sample of transfected cells, and monitoring the effect. The experiment includes a parallel sample which does not receive the candidate drug. The treated and untreated cells are then compared by any suitable phenotypic criteria, including but not limited to microscopic analysis, viability testing, ability to replicate, histological examination, the level of a particular RNA or polypeptide associated with the cells, the level of enzymatic activity expressed by the cells or cell lysates, and the ability of the cells to interact with other cells or compounds. Differences between treated and untreated cells indicates effects attributable to the candidate. In a preferred method, the effect of the drug on the cell transfected with the polynucleotide is also compared with the effect on a control cell. Suitable control cells include untransfected cells of similar ancestry, cells transfected with an alternative polynucleotide, or cells transfected with the same polynucleotide in an inoperative fashion. Optimally, the drug has a greater effect on operably transfected cells than on control cells.

25 30 Desirable effects of a candidate drug include an effect on any phenotype that was conferred by transfection of the cell line with the polynucleotide from the cancer-associated gene, or an effect that could limit a pathological feature of the gene in a cancerous cell. Examples of the first type would be a drug that limits the overabundance of RNA in the transfected cell, limits production of the encoded protein, or limits the functional effect of the protein. The effect of the drug would be apparent when comparing results between treated and untreated cells. An example of the second type would be a drug that makes use of the transfected gene or a gene product to specifically poison the cell. The effect of the drug would be apparent when comparing results between operably transfected cells and control cells.

*Use in treatment*

This invention also provides gene-specific pharmaceuticals in which each of the polynucleotides, polypeptides, and antibodies embodied herein as a specific active ingredient in pharmaceutical compositions. Such compositions may decrease the pathology of cancer cells on their own, or render the cancer cells more susceptible to treatment by the non-specific agents, such as classical chemotherapy or radiation.

An example of how polynucleotides embodied in this invention can be effectively used in treatment is gene therapy. See, for example, Morgan et al., Culver et al., and U.S. Patent No. 5,399,346 (French et al.). The general principle is to introduce the polynucleotide into a cancer cell in a patient, and allow it to interfere with the expression of the corresponding gene, such as by complexing with the gene itself or with the RNA transcribed from the gene. Entry into the cell is facilitated by suitable techniques known in the art as providing the polynucleotide in the form of a suitable vector, or encapsulation of the polynucleotide in a liposome. The polynucleotide may be provided to the cancer site by an antigen-specific homing mechanism, or by direct injection.

A preferred mode of gene therapy is to provide the polynucleotide in such a way that it will replicate inside the cell, enhancing and prolonging the interference effect. Thus, the polynucleotide is operably linked to a suitable promoter, such as the natural promoter of the corresponding gene, a heterologous promoter that is intrinsically active in cancer cells, or a heterologous promoter that can be induced by a suitable agent. Preferably, the construct is designed so that the polynucleotide sequence operably linked to the promoter is complementary to the sequence of the corresponding gene. Thus, once integrated into the cellular genome, the transcript of the administered polynucleotide will be complementary to the transcript of the gene, and capable of hybridizing with it. This approach is known as anti-sense therapy. See, for example, Culver et al. and Roth.

The use of antibodies embodied in this invention in the treatment of cancer partly relies on the fact that genes that show RNA overabundance in cancer frequently encode cell-surface proteins. Location of these proteins at the cell surface may correspond to an important biological function of the cancer cell, such as their interaction with other cells, the modulation of other cell-surface proteins, or triggering by an incoming cytokine.

These mechanisms suggest a variety of ways in which a specific antibody may be effective in decreasing the pathology of a cancer cell. For example, if the gene encodes for a growth receptor, then an antibody that blocks the ligand binding site or causes endocytosis of the receptor would decrease the ability of the receptor to provide its signal to the cell. It is unnecessary to have knowledge of the mechanism beforehand; the effectiveness of a particular antibody can be predicted empirically by testing with cultured cancer cells expressing the corresponding protein. Monoclonal antibodies may be more effective in this form of cancer therapy if several different clones directed at different determinants of the same cancer-associate gene product are used in combination: see PCT application WO 94/00136 (Kasprzyk et al.). Such antibody treatment may directly decrease the

pathology of the cancer cells, or render them more susceptible to non-specific cytotoxic agents such as platinum (Lippman).

Another example of how antibodies can be used in cancer therapy is in the specific targeting of effector components. The protein product of the cancer-associated gene is expected to appear in  
5 high frequency on cancer cells compared to unaffected cells, due to the overabundance of the corresponding RNA. The protein therefore provides a marker for cancer cells that a specific antibody can bind to. An effector component attached to the antibody therefore becomes concentrated near the cancer cells, improving the effect on those cells and decreasing the effect on non-cancer cells. This concentration would generally occur not only near the primary tumor, but also near cancer cells  
10 that have metastasized to other tissue sites. Furthermore, if the antibody is able to induce endocytosis, this will enhance entry of the effector into the cell interior.

For the purpose of targeting, an antibody specific for the protein of the cancer-associated gene is conjugated with a suitable effector component, preferably by a covalent or high-affinity bond. Suitable effector components in such compositions include radionuclides such as  $^{131}\text{I}$ , toxic chemicals  
15 such as vincristine, and toxic peptides such as diphtheria toxin. Other suitable effector components include peptides or polynucleotides capable of altering the phenotype of the cell in a desirable fashion: for example, installing a tumor suppresser gene, or rendering them susceptible to immune attack.

In most applications of antibody molecules in human therapy, it is preferable to use human monoclonals, or antibodies that have been humanized by techniques known in the art. This helps  
20 prevent the antibody molecules themselves from becoming a target of the host's immune system.

An example of how polypeptides embodied in this invention can be effectively used in treatment is through vaccination. The growth of cancer cells is naturally limited in part due to immune surveillance. This refers to the recognition of cancer cells by immune recognition units, particularly antibodies and T cells, and the consequent triggering of immune effector functions that limit tumor  
25 progression. Stimulation of the immune system using a particular tumor-specific antigen enhances the effect towards the tumor expressing the antigen. Thus, an active vaccine comprising a polypeptide encoded by the cDNA of this invention would be appropriately administered to subjects having overabundance of the corresponding RNA. There may also be a prophylactic role for the vaccine in a population predisposed for developing cancer cells with overabundance of the same  
30 RNA.

Ways of increasing the effectiveness of cancer vaccines are known in the art (Beardsley, MacLean et al.). For example, synthetic antigens are conjugated to a carrier like keyhole limpet hemocyanin (KLH), and then combined with an adjuvant such as DETOX™, a mixture of mycobacterial cell walls and lipid A. Any polypeptide encoded by the four novel genes described in  
35 this invention can be used in analogous compositions.

Methods for preparing and administering polypeptide vaccines are known in the art. Peptides may be capable of eliciting an immune response on their own, or they may be rendered more immunogenic by chemical manipulation, such as cross-linking or attaching to a protein carrier like KLH. Preferably, the vaccine also comprises an adjuvant, such as alum, muramyl dipeptides,

liposomes, or DETOX™. The vaccine may optionally comprise auxiliary substances such as wetting agents, emulsifying agents, and organic or inorganic salts or acids. It also comprises a pharmaceutically acceptable excipient which is compatible with the active ingredient and appropriate for the route of administration. The desired dose for peptide vaccines is generally from 10 µg to 1 mg, with a broad effective latitude. The vaccine is preferably administered first as a priming dose, and then again as a boosting dose, usually at least four weeks later. Further boosting doses may be given to enhance the effect. The dose and its timing are usually determined by the person responsible for the treatment.

#### 10 ***Sequence data and deposits***

The foregoing detailed description provides, inter alia, a detailed explanation of how genes associated with cancer can be identified and their cDNA obtained. Polynucleotide sequences for CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1 are provided.

15 The sequence data listed in this application was obtained by two-directional sequencing, except where indicated otherwise. The data are believed to be accurate — nevertheless, it is readily appreciated that the techniques of the art as used herein have the potential of introducing occasional and infrequent sequence errors. Clones and inserts obtained via PCR may also comprise occasional errors introduced during amplification. Nucleotide sequences predicted from database compilations, and sequence data obtained by one-directional sequencing may also contain occasional errors in accordance with the limitations of the underlying techniques. In addition, allelic variations to both nucleotide and amino acid sequences may occur naturally or be deliberately induced. Differences of any of these types between the sequences provided herein and the invention as practiced may be present without departing from the spirit of the invention.

25 Sequence data for CH8-2a13-1 and CH13-2a12-1 cDNA are believed to comprise the entire translated coding sequence, and 5' and 3' untranslated regions corresponding to those found in typical mRNA transcripts. Multiple mRNA transcripts may be found depending on the patterns of transcript processing in various cell types of interest. Sequence data for CH1-9a11-2 and CH14-2a16-1 cDNA comprise a portion of the coding sequence and 3' untranslated regions. Additional sequence is typically present in the corresponding mRNA transcripts, comprising an additional coding region in the N-terminal direction of the protein, and possibly a 5' untranslated region.

35 Certain embodiments of this invention may be practiced by polynucleotide synthesis according to the data provided herein, by rescuing an appropriate insert corresponding to the gene of interest from one of the deposits listed below, or by isolating a corresponding polynucleotide from a suitable tissue source. Various useful probes and primers for use in polynucleotide isolation are provided herein, or may be designed from the sequence data.



Three deposits have been made on May 31, 1996 with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852 under terms of the Budapest treaty. The deposits are outlined in Table 2:

TABLE 2: ATCC Deposits			
<b>BCGF1</b> Accession No. 98074	Mixture of <i>E. coli</i> with recombinant plasmids of cDNA fragments of genes associated with breast cancer. The 8 recombinant plasmids may be separated by plating on Ampicillin plates and selecting single colonies for analysis by PCR using SP6 and T7 primers.		
	Gene	Subclone	Expected size of PCR product
	CH1-9a11-2	pch1-1.1	1.1 kb
		pch1-2.5	2.5 kb
	CH8-2a13-1	pch8-600	600 bp
		pch8-3k	3.0 kb
		pch8-4k	4.0 kb
	CH14-2a16-1	pch14-800	800 kb
		pch14-1.6	1.6 kb
		pch14-1.3	1.3 kb
<b>BCGF 2</b> Accession No. 97595	Mixture of $\lambda$ gt10 recombinant phages with cDNA inserts of genes associated with breast cancer. The 2 phages may be separated by growing in the <i>E. coli</i> host (strain NM514) and plating out for single plaques. These plaques can be distinguished by PCR using $\lambda$ gt10 reverse and forward primers.		
	Gene	Phage	Expected size of PCR product
	CH13-2a12-1	$\lambda$ ch13-3.5	3.5 kb
	CH14-2a16-1	$\lambda$ ch14-2.5	2.5 kb
<b><math>\lambda</math>BCBT474</b> Accession No. 97594	cDNA library derived from breast cancer cell line BT474 in $\lambda$ gt10 vector, supplemented with a cDNA library from breast cancer cell line 600PE in $\lambda$ gt10 vector. The cDNA insert sizes range from about 0.5 to 5 kb. $\lambda$ BCBT474 is a source of additional cDNA inserts corresponding to CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, or CH14-2a16-1 not present in BCGF-1 or BCGF-2.		

5

Sequence databases contain sequences of polynucleotide and polypeptide fragments with various degrees of identity and overlap with certain embodiments of this invention. The following list of accession numbers is provided for the interest of the reader; it is not intended to be comprehensive or a limitation on the invention. The database disclosures do not typically indicate use in cancer

10

diagnosis, drug development, or disease treatment.

The following GenBank accession numbers are listed in relation to CH1-9a11-2: dbEST N32686; N45113; N36176; N22982; AA278830; H88670; AA235936; AA236951; H26301; N28026;

H88063; H88064; D61948; H88718; H26460; AA137920; AA145308; W12952; AA200687; N44164; T27279; dbSTS G22044; G04961.

The following GenBank accession numbers are listed in relation to CH8-2a13-1: dbNR D83780

5 The following GenBank accession numbers are listed in relation to CH13-2a12-1: dbNR U58090; dbEST AA182441; AA253924; AA179755; AA112715; AA112640; W67977; AA150317; W68080; AA150243; AA100446; W69636; H46574; AA245889; AA100651; H77368; AA192778; T85671; N32682; T86257; T78239; T77874; AA187866; Z33557; R40816; N99802; R19302; AA100650; N55904; AA257151; H77369; T79014.

10 The following GenBank accession numbers are listed in relation to CH14-2a16-1: dbEST N64802; W56903; N31400; W95674; AA233551; AA233636; N24105; W03447; W25821; AA233666; AA233647; N67843; D55778; T66839; N55370; N75650; AA280736; H97110; Z19643; H91250; AA230765; R93089; T84665; W94857; R92873

15 The examples presented below are provided as a further guide to a practitioner of ordinary skill in the art, and are not meant to be limiting in any way.

#### EXAMPLES

##### 20 *Example 1: Selecting cDNA for messenger RNA that is overabundant in breast cancer cells*

Total RNA was isolated from each breast cancer cell line or control cell by centrifugation through a gradient of guanidine isothiocyanate/CsCl. The RNA was treated with RNase-free DNase (Promega, Madison, WI). After extraction with phenol-chloroform, the RNA preparations were stored  
25 at -70°C. Oligo-dT polynucleotides for priming at the 3' end of messenger RNA with the sequence T<sub>11</sub>NM (where N ∈ {A,C,G} and M ∈ {A,C,G,T}) were synthesized according to standard protocols. Arbitrary decamer polynucleotides (OPA01 to OPA20) for priming towards the 5' end were purchased from Operon Biotechnology, Inc., Alameda, CA.

30 The RNA was reverse-transcribed using AMV reverse transcriptase (obtained from BRL) and an anchored oligo-dT primer in a volume of 20 μL, according to the manufacturer's directions. The reaction was incubated at 37°C for 60 min and stopped by incubating at 95°C for 5 min. The cDNA obtained was used immediately or stored frozen at -70°C.

Differential display was conducted according to the following procedure: 1 μL cDNA was replicated in a total volume of 10 μL PCR mixture containing the appropriate T<sub>11</sub>NM sequence, 0.5 μM of a decamer primer, 200 μM dNTP, 5 μCi [<sup>35</sup>S]-dATP (Amersham), Taq polymerase buffer with 2.5  
35 mM MgCl<sub>2</sub> and 0.3 unit Taq polymerase (Promega). Forty cycles were conducted in the following sequence: 94°C for 30 sec, 40°C for 2 min, 72°C for 30 sec; and then the sample was incubated at

72°C for 5 min. The replicated cDNA was separated on a 6% polyacrylamide sequencing gel. After electrophoresis, the gel was dried and exposed to X-ray film.

The autoradiogram was analyzed for labeled cDNA that was present in larger relative amount in all of the lanes corresponding to breast cancer cells, compared with all of the lanes corresponding to control cells. Figure 1 provides an example of an autoradiogram from such an experiment. Lane 5  
1 is from non-proliferating normal breast cells; lane 2 is from proliferating normal breast cells; lanes 3 to 5 are from breast cancer cell lines BT474, SKBR3, and MCF7. The left and right side shows the pattern obtained from experiments using the same T<sub>11</sub>NM sequence (T<sub>11</sub>AC), but two different decamer primers. The arrows indicate the cDNA fragments that were more abundant in all three  
10 tumor lines compared with controls.

The assay illustrated in Figure 1 was conducted using different combinations of oligo-dT primers and decamer primers. A number of differentially expressed bands were detected when different primer combinations were used. However, not all differences seen initially were reproducible after re-screening. We therefore routinely repeated each differential display for each  
15 primer combination. Only bands showing RNA overabundance in at least 2 experiments were selected for further analysis.

It is preferable to include in the differential display experiment RNA derived from uncultured normal mammary epithelial cells (termed "organoids"). These cells are obtained from surgical samples resected from healthy breast tissue, which are then coaxed apart by blunt dissection  
20 techniques and mild enzyme treatment. Using organoids as the negative control, 33 cDNA fragments were isolated from 15 displays.

***Example 2: Sub-selecting cDNA that corresponds to genes that are duplicated in breast cancer cells***

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cDNA fragments that were differentially expressed in the fashion described in Example 1 were excised from the dried gel and extracted by boiling at 95°C for 10 min. Eluted cDNA was recovered by ethanol precipitation, and replicated by PCR. The product was cloned into the pCRII vector using the TA cloning system (Invitrogen).

30

EcoRI digested placenta DNA, and EcoRI digested DNA from the breast cancer cell lines BT474, SKBR3 and ZR-75-30 were used to prepare Southern blots to screen the cloned cDNA fragments. The cloned cDNA fragments were labeled with [32P]-dCTP, and used individually to probe the blots. A larger relative amount of binding of the probe to the lanes corresponding to the cancer cell DNA indicated that the corresponding gene had been duplicated in the cancer cells. The labeled  
35 cDNA probes were also used in Northern blots to verify that the corresponding RNA was overabundant in the appropriate cell lines.

To determine whether the cDNA fragments obtained by this selection procedure corresponded to novel genes, a partial nucleotide sequence was obtained using M13 primers. Each sequence was compared with the known sequences in GenBank. In initial experiments, 5 of

the first 7 genes sequenced were mitochondrial genes. To avoid repeated isolation of mitochondrial genes, subsequent screening experiments were done with additional lanes in the DNA blot analysis for *EcoRI* digested and *HindIII* digested mitochondrial DNA. Any cDNA fragment that hybridized to the appropriate mitochondrial restriction fragments was suspected of corresponding to a mitochondrial gene, and not analyzed further.

From the 33 cDNA fragments detected from differential displays using organoid mRNA, 12 were subcloned. Of these 12, 6 detected suitable gene duplications in the appropriate cell lines. Three cDNA failed to detect duplicated genes, and 3 appeared to correspond to mitochondrial genes. Sequence analysis of the 6 suitable cDNA fragments showed no identity to any known genes.

To obtain longer cDNA corresponding to the cDNA fragments with novel sequences, the fragments were used as probes to screen a cDNA library from breast cancer cell line BT474, constructed in lambda GT10. The longer cDNA obtained from lambda GT10 were sequenced using lambda GT10 primers. The chromosomal locations of the cDNAs were determined using panels of somatic cell hybrids.

Four of the 6 novel cDNA identified so far have been processed in this fashion. The probes used to obtain the 4 new breast cancer genes are shown in Table 3.

TABLE 3: Primers used for Differential Display		
cDNA	Oligo-dT primer	Arbitrary primer
CH1-9a11-2	T <sub>11</sub> CC (SEQ ID NO: 9)	SEQ ID NO:11
CH8-2a13-1	T <sub>11</sub> AC (SEQ ID NO:10)	SEQ ID NO:12
CH13-2a12-1	T <sub>11</sub> AC (SEQ ID NO:10)	SEQ ID NO:13
CH14-2a16-1	T <sub>11</sub> AC (SEQ ID NO:10)	SEQ ID NO:14

### Example 3: Using the cDNA to test panels of breast cancer cells

To determine the proportion of breast cancers in which the putative breast cancer genes were duplicated, or showed RNA overabundance without gene duplication, the four cDNA obtained according to the selection procedures described were used to probe a panel of breast cancer cell lines and primary tumors.

Gene duplication was detected either by Southern analysis or slot-blot analysis. For Southern analysis, 10 µg of *EcoRI* digested genomic DNA from different cell lines was

electrophoresed on 0.8% agarose and transferred to a HYBOND™ N+ membrane (Amersham). The filters were hybridized with 32P-labeled cDNA for the putative breast cancer gene. After an autoradiogram was obtained, the probe was stripped and the blot was re-probed using a reference probe to adjust for differences in sample loading. Either chromosome 2 probe D2S5 or chromosome 21 probe D21S6 was used as a reference. Densities of the signals on the autoradiograms were obtained using a densitometer (Molecular Dynamics). The density ratio between the breast cancer gene and the reference gene was calculated for each sample. Two samples of placental DNA digests were run in each Southern analysis as a control.

For slot-blot analysis, 1 µg of genomic DNA was denatured and slotted on the HYBOND™ membrane. D21S5 or human repetitive sequences were used as reference probes for slot blots. The density ratio between the breast cancer gene and the reference gene was calculated for each sample. 10-15 samples of placental DNA digests were used as control. Amongst the control samples, the highest density ratio was set at 1.0. The density ratio of the tumor cell lines were standardized accordingly. An arbitrary cut-off for the standardized ratio (typically 1.3) was defined to identify samples in which the putative gene had been duplicated. Each of the cell lines in the breast cancer panel was scored positively or negatively for duplication of the gene being tested.

Some of the cell lines in the panel were known to have duplicated chromosomal regions from comparative genomic hybridization analysis. In instances where the cDNA being used as probe mapped to the known amplified region, the cDNA indicated that the corresponding gene had also been duplicated. However, duplicated genes were also detected using each of the four cDNAs in instances where comparative genomic hybridization had not revealed any amplification.

Because of the nature of the technique, the standardized ratio calculated as described underestimates the gene copy number, although it is expected to rank in the same order. For example, the standardized ratio obtained for the *c-myc* gene in the SKBR3 breast cancer cell was 5.0. However, it is known that SKBR3 has approximately 50 copies of the *c-myc* gene.

To test for overabundance of RNA, 10 µg of total RNA from breast cancer cell lines or primary breast cancer tumors were electrophoresed on 0.8% agarose in the presence of the denaturant formamide, and then transferred to a nylon membrane. The membrane was probed first with 32P-labeled cDNA corresponding to the putative breast cancer gene, then stripped and reprobed with 32P-labeled cDNA for the beta-actin gene to adjust for differences in sample loading. Ratios of densities between the candidate gene and the beta-actin gene were calculated. RNA from three different cultured normal epithelial cells were included in the analysis as a control for the normal level of gene expression. The highest ratio obtained from the normal cell samples was set at 1.0, and the ratios in the various tumor cells were standardized accordingly.

**Example 4: Chromosome 1 gene CH1-9a11-2**

One of the cDNA obtained through the selection procedures of Examples 1 and 2  
5 corresponded to a gene that mapped to Chromosome 1.

Table 4 summarizes the results of the analysis for gene duplication and RNA overabundance.

Both quantitative and qualitative assessment is shown. The numbers shown were obtained by  
comparing the autoradiograph intensity of the hybridizing band in each sample with that of the  
controls. Several control samples were used for the gene duplication experiments, consisting of  
10 different preparations of placental DNA. The control sample with the highest level of intensity was  
used for standardizing the other values. Other sources used for this analysis were breast cancer cell  
lines with the designations shown. For reasons stated in Example 3, the quantitative number is not a  
direct indication of the gene copy number, although it is expected to rank in the same order. Similarly,  
up to 6 control samples were used for the RNA overabundance experiments, consisting of different  
15 preparations of breast cell organoids which had been maintained briefly in tissue culture until the  
experiment was performed. The control sample with the highest level of intensity was used for  
standardizing the other values. Each cell line was scored + or - according to an arbitrary cut-off value.

TABLE 4: Chromosome 1 Gene In Breast Cancer Cell Lines						
Source	CH1-9a11-2 Gene Duplication		CH1-9a11-2 RNA Overabundance			
			5.2kb		4.4kb	
Normal	-	1.00*	-	1.00**	-	1.0**
BT474	+	2.70	+	1.57	+	3.7
ZR-75-30	+	2.65		nd		nd
MDA453	+	2.86	+	5.79	+	6.2
MDA435	+	3.72	-	0.89	+	2.4
SKBR3	+	1.86	-	0.94	+	2.9
600PE	+	1.72	+	4.47	+	6.8
MDA157	+	1.49	-	1.08	+	1.4
MCF7	+	1.95		nd		nd
DU4475	+	2.02	-	1.13	+	1.5
MDA231	-	1.23	+	1.47	-	
BT20	-	1.09	-	0.83	+	1.9
T47D	-	1.05		nd		nd
UACC812	-	0.67	+	1.57	+	1.8
MDA134	-	1.19	+	5.04	+	7.1
CAMA-1	-	1.02	+	2.51	+	7.2
Incidence (%)	9/15 (60%)		7/12 (58%)		11/12 (92%)	

Gene duplication or RNA overabundance; - no duplication or overabundance; nd = not done

\* Degree of gene duplication is reported relative to placental DNA preparations.

\*\* Degree of RNA overabundance is reported relative to the highest level observed for several cultures of normal epithelial cells. Two hybridizing species of RNA are calculated and reported separately.

The gene corresponding to the CH1-9a11-2 cDNA was duplicated in 9 out of 15 (60%) of the breast cancer cell lines tested, compared with placental DNA digests (P3 and P12). The sequence of the 115 bases from the 5' end of the cDNA fragment (SEQ. ID NO:1) is shown in Figure 22. There was no substantial homology to any known gene in GenBank. One of the three possible reading frames was found to be open, with the predicted amino acid shown in Figure 22 (SEQ. ID NO:2).

The CH1-9a11-2 gene was further characterized by obtaining additional sequence information. A  $\lambda$ -GT10 cDNA library from the breast cancer cell line BT474 (Example 2) was screened using the initial cDNA insert, and a clone with a 2.5 kilobase insert was identified. The identified clone was subcloned into plasmid vector pCRII. T7 and Sp6 primers for regions flanking the cDNA inserts were used as initial sequencing primers:

T7 primer: (SEQ. ID NO:42)

5'-TAATACGACTCACTATAGGGAGA-3'

Sp6 primer: (SEQ. ID NO:43)

5'-CATACGATTTAGGTGACACTATAG-3'

Sequencing continued by walking along the region of interest by standard techniques, using sequencing primers based on data already obtained. Primers used in sequencing are designated 1-16 in Figure 7.

A second clone (designated pCH1-1.1) overlapping on the 5' end was obtained using CLONTECH Marathon™ cDNA Amplification Kit. A map showing the overlapping regions is provided in Figure 6. Briefly, two DNA primers designated CH1a and CH1b (Figure 7) were synthesized. Polyadenylated RNA from breast cancer cell line 600PE was reverse transcribed using CH1b primer. After second strand synthesis, adaptor DNA provided in the kit was ligated to the double-stranded cDNA. The 5' end cDNA of CH1-9a11-2 was then amplified by PCR using primers CH1a and AP1 (provided in the kit). To increase the specificity of the PCR products, the first PCR products were PCR reamplified using nested primers CH1a and AP2 (provided in the kit). The PCR products were cloned into pCRII vector (Invitrogen) and screened with CH1-9a11-2 probe.

The sequence of 3452 base pairs between the 5' end of pCH1-1.1 and the poly-A tail of CH1-9a11-2 was determined by standard sequencing techniques. The DNA sequence is shown in Figure 8 (SEQ. ID NO:15). The longest open reading frame is in frame 1 (bases 1-1875), and codes for 624 amino acids before the stop codon. The corresponding amino acid sequence of this frame is shown in the upper panel of Figure 9 (SEQ. ID NO:16). The partial sequence predicted for the translated protein is listed the low panel of Figure 9 (SEQ. ID NO:17). Bases 1876 to the end of the sequence are believed to be a 3' untranslated region. A hydrophobicity analysis identified a putative membrane insertion or membrane spanning region at about amino acids 382-400, indicated in Figure 9 by underlining.

Figure 23 is a listing of additional cDNA sequence obtained for CH1-9a11-2, comprising approximately 1934 base pairs 5' from the sequence of Figure 8. The additional sequence data was obtained by rescuing and amplifying two further fragments of CH1-9a11-2 cDNA. Nested primers were designed ~100 base pairs downstream from the 5' end of the known sequence. The primers were used in a nested amplification assay using AP1 and AP2, using the CLONTECH Marathon™ cDNA Amplification Kit as described above. The template for the first upstream fragment was reverse-transcribed polyadenylated RNA from breast cancer cell line 600PE, as described earlier.



This fragment was sequenced, and another set of nested primers was designed. The template for the next upstream fragment was a Marathon™ ready cDNA preparation from human testes, also supplied by CLONTECH.

5 The nucleotide sequence shown in Figure 23 comprises an open reading frame through to the 5' end. Figure 24 shows the corresponding protein translation. Between about another 500-1000 bases are predicted to be present in the CH1-9a11-2 direction, with the protein encoding sequence beginning somewhere within this additional sequence. Sequencing of the encoding region is completed by obtaining additional CH1-9a11-2 fragments in this direction.

10 A GENINFO® BLAST search of nucleotide and peptide sequence databases was performed through the National Center for Biotechnology Information on February 23, 1996. Short segments of homology with other reported human sequences were found at the nucleotide level (<500 base pairs), but none with any ascribed function in the respective identifier. At the amino acid level, no identity higher than 30% was found with any reported eukaryotic sequences.

15 A CH1-9a11-2 cloned insert has been used to probe the level of relative expression in polyadenylated RNA from a panel of tissue sources. The RNA was obtained already prepared for Northern blot analysis (CLONTECH Catalog # 7759-1, 7760-1 and 7756-1.) The manufacturer produced the blots from approximately 2 µg of poly-A RNA per lane, run on a denaturing formaldehyde 1-2% agarose gel, transferred to a nylon membrane, and fixed by UV irradiation. The relative CH1-9a11-2 expression observed at the RNA level is shown in Table 5:

20

TABLE 5: Northern blot analysis	
Tissue	CH1-9a11-2 mRNA
heart	++
brain	+
placenta	++
lung	+/-
liver	+/-
skeletal muscle	+
kidney	+/-
pancreas	+++
spleen	+
thymus	+
prostate	++
testis	+++
ovary	++
small intestine	+
colon	+/-
peripheral blood	+/-
++++ Very high +++ High ++ Medium + Low +/- Very low	

Relatively elevated levels of expression were observed in heart, placenta, pancreas, prostate, testis and ovary. The level of expression in breast cancer cell lines is also relatively high (about ++++ on the scale), since the Northern analysis performed on these lines (described above) was conducted on  
 5 *total* cellular RNA, of which polyadenylated RNA constitutes only about 5%. It is likely that the CH1-9a11-2 gene is involved in a biological process that is typical to the tissue types showing medium to high levels of expression, which may relate to increased tissue growth or metabolism.

Since the obtained sequence is shorter than the apparent size of mRNA observed in Northern analysis (Table 1), an additional polynucleotide segment is believed to be present at the 5' end of the sequence shown in SEQ. ID NO:15. Further sequence data at the 5' end is deduced by  
 10 obtaining additional cloned cDNA using standard techniques. Briefly, in one approach, mRNA from breast cancer cell lines MDA-453 and/or 600PE are cloned and screened using primers based on sequence data from SEQ. ID NO:15. Two nested primers of about 20 nucleotides are prepared, the innermost about 150 base pairs from the 5' end, and the outermost about 170 base pairs from the 5' end. The outermost primer is used to synthesize a first cDNA strand complementary to the mRNA in  
 15 the upstream direction. Second strand synthesis is performed using reagents in a CLONTECH

Marathon™ cDNA amplification kit according to manufacturer's directions. The double-stranded DNA is then ligated at the 5' end of the coding sequence with the double-stranded adaptor fragment provided in the kit. A first PCR amplification (about 30 cycles) is performed using the first adapter primer from the kit and the outermost RNA-specific primer, and a second amplification (about 30 cycles) is performed using the second adapter primer and the innermost RNA-specific primer. In an alternative approach, a CLONTECH RACE-READY single-stranded cDNA from human placenta is PCR amplified using nested 5' anchor primers in combination with the outermost and innermost RNA-specific primers. Amplified DNA obtained using either approach is analyzed by gel electrophoresis, and cloned into plasmid vector pCRII. Clones are screened, as necessary, using the 2.5 kilobase CH1-9a11-2 insert. Clones corresponding to full-length mRNA (4.5 kb or 5.5 kb; Table 1), or cDNA fragments overlapping at the 5' end are selected for sequencing. Compared with the 4.5 kb form, additional polynucleotide segments may be present in the 5.5 kb form within the encoding region, or in the 5' or 3' untranslated region.

**Example 5: Chromosome 8 gene CH8-2a13-1**

One of the cDNA obtained corresponded to a gene that mapped to Chromosome 8. Figure 2 shows the Southern blot analysis for the corresponding gene in various DNA digests. Lane 1 (P12) is the control preparation of placental DNA; the rest show DNA obtained from human breast cancer cell lines. Panel A shows the pattern obtained using the 32P-labeled CH8-2a13-1 cDNA probe. Panel B shows the pattern obtained with the same blot using the 32P-labeled D2S6 probe as a loading control. The sizes of the restriction fragments are indicated on the right.

Figure 3 shows the Northern blot analysis for RNA overabundance. Lanes 1-3 show the level of expression in cultured normal epithelial cells. Lanes 4-19 show the level of expression in human breast cancer cell lines. Panel A shows the pattern obtained using the CH8-2a13-1 probe; panel B shows the pattern obtained with beta-actin cDNA, a loading control.

The results are summarized in Table 6. The scoring method is the same as for Example 4.

TABLE 6: Chromosome 8 Genes In Breast Cancer Cell Lines						
Source	CH8-2a13-1 Gene Duplication		CH8-2a13-1 RNA Overabundance		c-myc Gene Duplication	
Normal	-	1.00*	-	1.00**	-	1.00*
SKBR3	+	4.25	+	4.30	+	4.73
ZR-75-30	+	3.82	nd		+	2.24
BT474	+	1.53	+	1.72	+	1.76
MDA157	+	2.02	+	3.39	+	1.39
MCF7	+	1.84	+	4.92	+	3.10
CAMA-1	+	3.62	+	2.14	+	1.61
MDA361	+	2.00	+	1.74	nd	
MDA468	nd		+	4.50	nd	
T47D	+	1.41	+	1.58	-	1.02
MDA453	+	1.83	+	3.10	-	0.90
MDA134	+	1.30	+	3.70	-	0.88
MDA435	+	2.15	+	4.94	-	1.00
600PE	-	0.95	+	2.04	-	0.54
UACC812	+	1.25	+	2.40	-	0.74
MDA231	-	0.80	+	1.28	+	1.27
DU4475	-	0.85	-	0.88	-	0.50
BT468	-	0.37	-	0.70	-	0.23
BT20	-	0.95	-	0.82	-	
Incidence (%)	12/17 (71%)		14/17 (82%)		7/16 (44%)	

- + Gene duplication or RNA overabundance; - no duplication or overabundance; nd = not done.  
 \* Degree of gene duplication is reported relative to placental DNA preparations.  
 \*\* Degree of RNA overabundance is reported relative to the highest level observed for several cultures of normal epithelial cells.

5

The gene corresponding to CH8-2a13-1 showed clear evidence of duplication in 12 out of 17 (71%) of the cells tested. RNA overabundance was observed in 14 out of 17 (82%). Thus, 11% of the cells had achieved RNA overabundance by a mechanism other than gene duplication.

10

Since the known oncogene c-myc is located on Chromosome 8, the Southern analysis was also conducted using a probe for c-myc. At least 2 of the breast cancer cells showing duplication of the gene corresponding to CH8-2a13-1 gene did not show duplication of c-myc. This indicates that the gene corresponding to CH8-2a13-1 is not part of the myc amplicon.

The sequence of 150 bases from the 5' end of the cDNA fragment is shown in Figure 22 (SEQ ID NO:3). There was no substantial homology to any known gene in GenBank. One of the

15

three possible reading frames was found to be open, with the amino acid sequence shown in Figure 22 (SEQ ID NO:4).

The CH8-2a13-1 gene was further characterized by obtaining additional sequence information. A  $\lambda$ -GT10 cDNA library from the breast cancer cell line BT474 (Example 2) was screened using the initial cDNA insert, and clones with a 3.0 kb and a 4.0 kb insert were identified. The two identified clones were subcloned into plasmid vector pCRII. T7 and Sp6 primers for regions flanking the cDNA inserts were used as initial sequencing primers. Sequencing continued by walking along the region of interest by standard techniques, using sequencing primers based on data already obtained. The two inserts were found to overlap (Figure 6). Primers used are those designated 1-25 in Figure 10.

A third clone of about 600 bp (designated pCH8-600) overlapping on the 5' end (Figure 6) was obtained using CLONTECH Marathon™ cDNA Amplification Kit. Briefly, two DNA primers CH8a and CH8b (Figure 10) were synthesized. Polyadenylated RNA from breast cancer cell line BT474 was reverse transcribed using CH8b primer. After second strand synthesis, adaptor DNA provided in the kit was ligated to the double-stranded cDNA. The 5' end cDNA of CH8-2a13-1 was then amplified by PCR using primers CH8a and AP1 (provided in the kit). To increase the specificity of the PCR products, the first PCR products were PCR reamplified using nested primers CH8a and AP2 (provided in the kit). The PCR products were cloned into pCRII vector (Invitrogen) and screened with CH8-2a13-1 probe.

By sequencing relevant portions of the three clones, a nucleic acid sequence of 3982 base pairs between the 5' end and the poly-A tail of CH8-2a13-1 was determined. The DNA sequence is shown in Figure 11 (SEQ. ID NO:18). Bases 1-152 are believed to be a 5' untranslated region. The longest open reading frame is in frame 3 from base 153 to 3911, and codes for 1252 amino acids before the stop codon. The corresponding amino acid sequence of this frame is shown in the upper panel of Figure 12 (SEQ. ID NO:19). The sequence predicted for the translated protein is shown in the lower panel of Figure 12 (SEQ. ID NO:20).

A GENINFO® BLAST search of nucleotide and peptide sequence databases was performed through the National Center for Biotechnology Information on March 26, 1996. The sequences were found to be about 99% identical at the nucleotide and amino acid level with bases 343-4103 of KIAA0196 protein (N. Nomura et al., in press; sequence submitted to the DDBJ/EMBL/GenBank databases on March 4, 1996). The KIAA0196 was one of 200 different cDNA cloned at random from an immature male human myeloblast cell line. KIAA0196 has no known biological function, and is described by Nomura et al. as being ubiquitously expressed.

A fourth clone of about 600 bp overlapping pCH8-600 at the 5' end has also been obtained. Briefly, a DNA primer was synthesized corresponding to about the first 20 nucleotides at the 5' of the predicted cDNA sequence, and used along with a primer based on the pCH8-600 sequence to reverse-transcribe RNA from breast cancer cell line BT474. The product was cloned into pCRII vector (Invitrogen) and screened with a CH8-2a13-1 probe. The new clone is sequenced along both strands to obtain additional 5' untranslated sequence data for the cDNA. The predicted compiled cDNA

nucleotide sequence of CH8-2a13-1 cDNA is shown in Figure 13 (SEQ. ID NO:21). The corresponding amino acid sequence of this frame is shown in Figure 14 (SEQ. ID NO:22). A polynucleotide comprising the compiled sequence is assembled by joining the insert of this fourth clone to pCH8-4k within the shared region. Briefly, CH8-4k is cut with *Xba*I and *Not*I. The fourth clone is cut with *Bam*HI and *Xba*I. The ligated polynucleotide is then inserted into pCRII cut with *Bam*HI and *Not*I.

A CH8-2a13-1 cloned insert has been used to probe the level of relative expression in polyadenylated RNA from a panel of tissue sources obtained from CLONTECH, as in Example 4. The relative CH8-2a13-12 expression observed at the mRNA level is shown in Table 7:

10

TABLE 7: Northern blot analysis	
Tissue	CH1-9a11-2 mRNA
heart	++
brain	+
placenta	+
lung	+
liver	+/-
skeletal muscle	+/-
kidney	+/-
pancreas	+/-
spleen	+
thymus	+
prostate	+
testis	++
ovary	+
small intestine	+
colon	+
peripheral blood	+/-
++++ Very high +++ High ++ Medium + Low +/- Very low	

Relative levels of expression observed were as follows: Low levels of expression were observed in adult peripheral blood leukocytes (PBL), brain, placenta, lung, liver, skeletal muscle, kidney, and pancreas. Medium levels of expression were observed in adult heart, spleen, thymus, prostate, testis, ovary, small intestine, and colon. High levels of expression were observed in four fetal tissues tested: brain, lung, liver and kidney. The level of expression in breast cancer cell lines is relatively high

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(about ++++ on the scale), since the Northern analysis performed on these lines was conducted on *total* cellular RNA. It is likely that the CH8-2a13-1 gene is involved in a biological process that is typical to the tissue types showing medium to high levels of expression, which may relate to increased tissue growth or metabolism.

5

**Example 6: Chromosome 13 gene CH13-2a12-1**

One of the cDNA obtained corresponded to a gene that mapped to Chromosome 13. Figure 4 shows the Southern blot analysis for the corresponding gene in various DNA digests. Lanes 1 and 2 are control preparations of placental DNA; the rest show DNA obtained from human breast cancer cell lines. Panel A shows the pattern obtained using the CH13-2a12-1 cDNA probe; panel B shows the pattern using D2S6 probe as a loading control. The sizes of the restriction fragments are indicated on the right.

Figure 5 shows the Northern blot analysis for RNA overabundance of the CH13-2a12-1 gene. Lanes 1-3 show the level of expression in cultured normal epithelial cells. Lanes 4-19 show the level of expression in human breast cancer cell lines. Panel A shows the pattern obtained using the CH13-2a12-1 probe; panel B shows the pattern obtained with beta-actin cDNA, a loading control. The apparent size of the mRNA varied depending upon conditions of electrophoresis. Full-length mRNA is believed to occur at sizes of about 3.2 and 3.5 kb.

The results of the RNA abundance comparison are summarized in Table 8. The scoring method is the same as for Example 4.

TABLE 8: Chromosome 13 Gene In Breast Cancer Cell Lines		
Source	CH13-2a12-1 Gene duplication	CH13-2a12-1 RNA Overabundance
Normal	- 1.00*	- 1.00**
600PE	+ 2.18	+ 5.57
BT474	+ 1.60	+ 3.20
SKBR3	+ 1.58	+ 4.25
MDA157	+ 2.21	+ 3.76
CAMA-1	+ 1.41	+ 1.99
MDA231	+ 1.65	+ 2.09
T47D	+ 1.23	+ 1.20
MDA468	nd	+ 6.90
MDA381	nd	+ 2.59
MDA435	- 0.59	+ 3.41
MDA134	- 0.53	+ 2.59
DU4475	- 0.75	+ 1.79
MDA453	- 0.89	+ 1.97
BT20	- 0.37	- 1.04
MCF7	- 0.29	- 1.03
UACC812	- 0.30	- 0.39
BT468	- 0.47	nd
ZR-75-30	- 0.70	nd
Incidence (%)	7/16 (44%)	13/16 (81%)

- + Gene duplication or RNA overabundance; - no duplication or overabundance; nd = not done  
 \* Degree of gene duplication is reported relative to placental DNA preparations.  
 \*\* Degree of RNA overabundance is reported relative to the highest level observed for several cultures of normal epithelial cells.

5

The gene corresponding to CH13-2a12-1 was duplicated in 7 out of 16 (44%) of the cells tested. Three of the positive cell lines (600PE, BT474, and MDA435) had been studied previously by comparative genomic hybridization, but had not shown amplified chromatin in the region where CH13-2A12-1 has been mapped in these studies.

10

RNA overabundance was observed in 13 out of 16 (81%) of the cell lines tested. Thus, 37% of the cells had achieved RNA overabundance by a mechanism other than gene duplication.



Cells from primary breast tumors have also been analyzed them for duplication of the chromosome 13 gene. Ten of the 82 tumors analyzed (12%) were positive, confirming that duplication of this gene is not an artifact of in vitro culture.

5 The sequence of 107 bases from the 5' end of the 1.5 kb cDNA fragment is shown in Figure 22 (SEQ ID NO:5). There was no substantial homology to any known gene in GenBank. One of the three possible reading frames was found to be open, with the predicted amino acid sequence shown in Figure 22 (SEQ ID NO:6).

10 The CH13-2a12-1 gene was further characterized by obtaining additional sequence information. A  $\lambda$ -GT10 cDNA library from the breast cancer cell line BT474 (Example 2) was screened using the initial cDNA insert, and clones with a 3.5 kilobase and a 1.6 kilobase insert were identified. The two identified clones were subcloned into plasmid vector pCRII. T7 and Sp6 primers for regions flanking the cDNA inserts were used as initial sequencing primers. Sequencing continued by walking along the region of interest by standard techniques, using sequencing primers based on data already obtained. The two inserts were found to overlap (Figure 6). Primers used during  
15 sequencing are shown in Figure 15.

By sequencing relevant portions of the 3.5 and 1.6 kb clones, a nucleic acid sequence of 3339 base pairs between the 5' end and the poly-A tail of CH13-2a12-1 was determined. The DNA sequence is shown in Figure 16 (SEQ. ID NO:23). Bases 1-520 are believed to be a 5' untranslated region. The longest open reading frame is in frame 2 from base 521 to 1838, and codes for 611  
20 amino acids before the stop codon. The corresponding amino acid sequence of this frame is shown in the upper panel of Figure 17 (SEQ. ID NO:24). The sequence predicted for the translated protein is shown in the lower panel of Figure 17 (SEQ. ID NO:25). Bases 1838 to 3339 of the nucleotide sequence are believed to be a 3' untranslated region, which is present in the 3.5 kb insert. The 3.5 kb insert appears to be a splice variant (Figure 6), in which the 3' untranslated region consists of bases  
25 1838-2797 in the sequence.

A GENINFO® BLAST search of nucleotide and peptide sequence databases was performed through the National Center for Biotechnology Information on March 26, 1996. Short segments of homology with other reported human sequences were found at the nucleotide level (<500 base pairs), but none with any ascribed function in the respective identifier. At the amino acid level, the sequence  
30 was found to share 33% identities and 54% positives with 228 residues of the *lin 19* protein of *Caenorhabditis elegans*. This protein has been implicated in regulating the cell cycle of *C. elegans* (ET Kiprecs, W He & EM Hedgecock). The CH13-2a12-1 gene is suspected of a role in controlling cell proliferation. "Controlling cell proliferation" in this context means that an abnormally high or low level of gene expression at the RNA or protein level results in a higher or lower rate of cell  
35 proliferation, or vice versa, compared with cells with an otherwise similar phenotype. There is also a low-level homology between CH13-2a12-1 and VACM-1, a vasopressin-activated, calcium-mobilizing receptor from rabbit kidney medulla (Burnatowska-Hledin et al). VACM-1 has a transmembrane

sequence, whereas none has been detected in CH13-2a12-1. Nevertheless, it is possible that the CH13-2a12-1 protein product has a  $\text{Ca}^{++}$  binding or  $\text{Ca}^{++}$  mobilizing function.

A CH13-2a12-1 cloned insert has been used to probe the level of relative expression in polyadenylated RNA from a panel of tissue sources obtained from CLONTECH, as in Example 4.

- 5 The relative CH13-2a12-1 expression observed at the mRNA level is shown in Table 9:

TABLE 9: Northern blot analysis	
Tissue	CH13-2a12-1 mRNA
heart	++++
brain	+
placenta	++
lung	+
liver	++
skeletal muscle	++++
kidney	+
pancreas	++
spleen	++
thymus	++
prostate	++
testis	+++
ovary	++
small intestine	++
colon	+
peripheral blood	+
++++ Very high +++ High ++ Medium + Low +/- Very low	

- Relatively elevated levels of expression were observed in heart, skeletal muscle and testis. The level of expression in breast cancer cell lines is relatively high (about ++++ on the scale), since the Northern analysis performed on these lines was conducted on *total* cellular RNA. It is likely that the CH13-2a12-1 gene is involved in a biological process that is typical to the tissue types showing medium to high levels of expression, which may relate to increased tissue growth or metabolism.

- Fragments corresponding to the CH13-2a12-1 gene have also been used to screen cell lines derived from other types of cancer. Southern analysis showed that about 1 out of 4 breast cancer cell lines tested have gene duplication of CH13-2a12-1. Northern analysis showed that about 3 out of 6 lines tested have overexpression of the corresponding RNA transcript.

**Example 7: Chromosome 14 gene CH14-2a16-1**

One of the cDNA obtained corresponded to a gene that mapped to Chromosome 14. Results  
 5 of the analysis are summarized in Table 10. The scoring method is the same as for Example 4.

<b>TABLE 10: Chromosome 14 Gene in Breast Cancer Cell Lines</b>		
<b>Source</b>	<b>CH14-2a16-1 Gene duplication</b>	<b>CH14-2a16-1 RNA Overabundance</b>
Normal	- 1.00*	- 1.00**
BT474	+ 2.89	+ 2.57
MCF7	+ 1.35	+ 1.88
SKBR3	+ 2.58	+ 2.19
T47D	+ 2.28	nd
MDA157	+ 1.52	+ 2.52
UACC812	+ 2.23	nd
MDA361	- 0.97	+ 1.43
MDA453	+ 1.58	+ 5.92
BT20	-	- 1.07
600PE	- 0.94	+ 2.00
MDA231	+ 1.66	+ 2.19
CAMA-1	- 0.92	- 0.71
DU4475	- 0.87	+ 1.33
BT468	- 0.46	nd
MDA134	- 0.77	+ 7.17
<b>Incidence (%)</b>	<b>8/15 (53%)</b>	<b>10/12 (83%)</b>

+ Gene duplication or overabundance; - no duplication or overabundance; nd = not done

\* Degree of gene duplication is reported relative to placental DNA preparations.

\*\* Degree of RNA overabundance is reported relative to the highest level observed for several cultures of normal epithelial cells.

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The gene corresponding to CH14-2a16-1 was duplicated in 8 out of 15 (53%) of the cells tested. The sequence of 114 bases from the 5' end of the cDNA fragment is shown in Figure 22 (SEQ ID NO:7). There was no substantial homology to any known gene in GenBank. One of the three possible reading frames was found to be open, with the predicted amino acid sequence shown in Figure 22 (SEQ ID NO:8).

The CH14-2a16-1 gene was further characterized by obtaining additional sequence information. A  $\lambda$ -GT10 cDNA library from the breast cancer cell line BT474 (Example 2) was screened using the initial cDNA insert, and two clones were identified: one with a 1.6 kb insert, and the other with a 2.5 kb insert. The identified clones were subcloned into plasmid vector pCRII. The 1.6 kb insert was sequenced by using T7 and Sp6 primers for regions flanking the cDNA inserts as initial sequencing primers. Sequencing continued by walking along the region of interest by standard techniques, using sequencing primers based on data already obtained. Primers used are those designated 1-11 in Figure 18.

A third clone (designated pCH14-800) overlapping on the 5' end (Figure 6) was obtained using CLONTECH Marathon™ cDNA Amplification Kit. Briefly, DNA primers CH14a, CH14b, CH14c and CH14d (Figure 18) were prepared. Polyadenylated RNA from breast cancer cell line MDA453 was reverse transcribed using 14b primer. After second strand synthesis, adaptor DNA provided in the kit was ligated to the double-stranded cDNA. The 5' end cDNA of CH14-2a16-1 was then amplified by PCR using primers CH14b (or CH14c) and AP1 (provided in the kit). To increase the specificity of the PCR products, the first PCR products were PCR reamplified using nested primers CH14a (or CH14d) and AP2 (provided in the kit). The PCR products were cloned into pCRII vector (Invitrogen) and screened with CH14-2a16-1 probe.

By sequencing pCH14-1.6 and pCH14-800, a nucleic acid sequence of 2021 base pairs between the 5' end and the poly-A tail of CH14-2a16-1 has been determined. The DNA sequence is shown in Figure 19 (SEQ. ID NO:26). The longest open reading frame is in frame 1 from base 1 to 792, and codes for 263 amino acids before the stop codon. The corresponding amino acid sequence of this frame is shown in the upper panel of Figure 20 (SEQ. ID NO:27). The partial sequence predicted for the translated protein is shown in the lower panel of Figure 20 (SEQ. ID NO:28). The 2.1 kb clone has not been sequenced, but is believed to consist about the same region of the CH14-2a16-1 cDNA as pCH14-1.6 and pCH14-800 combined.

A GENINFO® BLAST search of nucleotide and peptide sequence databases was performed through the National Center for Biotechnology Information on March 26, 1996. Short segments of homology with other reported human sequences were found at the nucleotide level (<500 base pairs), but none with any ascribed function in the respective identifier. At the amino acid level, the sequence was found to share homologies within the first 106 residues with an RNA binding protein from *Saccharomyces cerevisiae* with the designation NAB2. NAB2 is one of the major proteins associated with nuclear polyadenylated RNA in yeast cells, as detected by UV light-induced cross-linking and immunofluorescence. NAB2 is strongly and specifically associated with nuclear poly(A)<sup>+</sup> RNA in vivo.

Gene knock-out experiments have shown that this protein is essential to yeast cell survival (Anderson et al.). Accordingly, the protein encoded by CH14-2a16-1 is suspected of having DNA or RNA binding activity.

A fourth clone (pCH14-1.3) has been obtained that overlaps the pCH14-800 clone at the 5' end (Figure 6). The method of isolation was similar to that for pCH14-800, using primers based on the pCH14-800 sequence. Partial sequence data for pCH14-1.3 has been obtained by one-

directional sequencing from the 5' and 3' ends of the pCH14-1.3 clone. Figure 21 shows the nucleotide sequence of the sequence of the 5' end (SEQ. ID NO:29) and the amino acid translation of the likely open reading frame (SEQ. ID NO:30); the nucleotide sequence of the 3' end (SEQ. ID NO:31) and the likely open reading frame (SEQ. ID NO:32). This data is confirmed and additional sequence between SEQ. ID NOS.29 and 31 is obtained by fully sequencing both strands of pCH14-1.3. Once compiled, the sequence data from pCH14-1.3, pCH14-800 and pCH14-1.6 may be shorter than the apparent size of mRNA observed in Northern analysis (Table 1). If necessary, further sequence data at the 5' end is deduced by obtaining additional cloned cDNA according to approaches described in this Example or Example 4.

Figure 25 is a listing of additional cDNA sequence obtained for CH14-2a16-1, comprising approximately 1934 base pairs 5' from the sequence of Figure 19. The corresponding amino acid translation is shown in the upper panel of Figure 26. The additional sequence data was obtained by rescuing and amplifying further fragments of CH14-2a16-1 cDNA. Nested primers were designed ~100 base pairs downstream from the 5' end of the known sequence. The primers were used in a nested amplification assay using AP1 and AP2, using the CLONTECH Marathon™ cDNA Amplification Kit as described above. The template was a Marathon™ ready cDNA preparation from human testes, also supplied by CLONTECH.

The nucleotide sequence shown in Figure 25 is closed at the the 5' end. The lower panel of Figure 26 shows what is predicted to be the sequence of the gene product, beginning at the first methionine residue. The nucleotide sequence shown contains a point difference at the position indicated by the underlining in Figure 25. A base determined to be A from the previously obtained polynucleotide fragment was a G in the one used in this part of the experiment. This corresponds to a change from E (glutamic acid) to G (glycine) in the protein sequence, at the position underlined in Figure 26. This may represent a natural allelic variation.

A CH14-2a16-1 cloned insert has been used to probe the level of relative expression in polyadenylated RNA from a panel of tissue sources obtained from CLONTECH, as in Example 4. The relative CH14-2a16-1 expression observed at the mRNA level is shown in Table 11:

TABLE 11: Northern blot analysis	
Tissue	CH14-2a16-1 mRNA
heart	+
brain	+
placenta	+
lung	+
liver	+
skeletal muscle	+
kidney	+/-
pancreas	+
spleen	+
thymus	+
prostate	+
testis	++++
ovary	+
small intestine	+
colon	+
peripheral blood	+/
+++++ Very high ++++ High ++ Medium + Low +/- Very low	

CH14-2a16-1 mRNA was particularly high in testis. The level of expression in breast cancer cell lines is also quite high, since the Northern analysis performed on these lines was conducted on total cellular RNA. It is likely that the CH14-2a16-1 gene is involved in a biological process that is typical to the tissue types showing medium to high levels of expression, which may relate to increased tissue growth or metabolism.

Five motifs corresponding to a zinc finger protein have been found in the CH14-2a16-1 nucleotide sequence. Further zinc finger motifs may be present in CH14-2a16-1 in the upstream direction. Zinc finger motifs are present, for example, in RNA polymerases I, II, and III from *S. cerevisiae*, and are related to the zinc knuckle family of RNA/ssDNA-binding proteins found in the HIV nucleocapsid protein. The actual sequence observed in each of the five zinc finger motifs of CH14-2a16-1 is:

Cys-(Xaa)<sub>5</sub>-Cys-(Xaa)<sub>4</sub>-Cys-(Xaa)<sub>3</sub>-His or (SEQ. ID NO:38)  
 Cys-(Xaa)<sub>5</sub>-Cys-(Xaa)<sub>5</sub>-Cys-(Xaa)<sub>3</sub>-His (SEQ. ID NO:39)

which is indicated in Figure 20 by underlining. This is identical to the 7 zinc finger motifs of NAB2, which make up an RNA/ssDNA binding region (Anderson et al.). Accordingly, the CH14-2a16-1 gene product is suspected of having DNA or RNA binding activity, and may be specific for polyadenylated RNA. It may very well play a role in the regulation of gene replication, transcription, the processing of hnRNA into mature mRNA, the export of mRNA from the nucleus to the cytoplasm, or translation into protein. This role in turn may be closely implicated in cell growth or proliferation, particularly as manifest in tumor cells.

**Example 8: Identification of other cancer-associated genes**

cDNA fragments corresponding to additional cancer-associated genes are obtained by applying the techniques of Examples 1 & 2 with appropriate adaptations. As before, cancer cells are selected for use in differential display of RNA, based on whether they share a duplicated chromosomal region according to Table 12:

TABLE 12: Cancer cell lines sharing duplicated chromosomal regions	
Chromosomal location	Cancer type & references
1p22-32	small cell (Levin 1994)
1p22	bladder (Kallioniemi 1995)
1p32-33	rhabdomyosarcoma (Steilen-Gimbel); breast (Ried 1995); small cell lung (Ried 1994)
1q21-22	sarcoma (Forus 1995a & b); breast (Muleris 1994a)
1q24	small cell (Levin 1994)
1q31	bladder (Kallioniemi 1995)
1q32	glioma (Muleris 1994b; Schrock)
1q	head and neck (Speicher 1995), breast (Muleris 1994a)
2p23	small cell lung (Ried 1994)
2p24-25	small cell lung (Levin 1994)
2	head and neck (Speicher 1995)
2q	head and neck (Speicher 1995)
2q33-36	head and neck (Speicher 1995)
3p22-24	bladder (Voorter), small cell (Levin 1994)
3q24-26	bladder (Kallioniemi 1995), glioma (Kim), osteosarcoma (Tarkkanen)
3q25-26	ovarian (Iwabuchi)

TABLE 12: Cancer cell lines sharing duplicated chromosomal regions	
Chromosomal location	Cancer type & references
3q26-term	head and neck (Speicher 1995)
3q	small cell lung (Levin 1995; Ried 1994); head and neck (Speicher 1995)
4q12	glioma (Schrock)
5p	small cell lung (Levin 1994 & 1995; Ried 1994)
5p15.1	glioma (Muleris 1994b)
6p	osteosarcoma (Forus 1995a); breast (Ried 1995)
6p21-term	melanoma (Speicher)
7p	glioma (Schliegel 1994 & 1996; may be EGFR)
7p11-12	glioma (Muleris 1994b; Schrock), small cell lung (Ried 1994)
7q21-32	glioma (Kim; Muleris 1994b; Schrock)
7q21-22	head and neck (Speicher), glioma (Schrock)
7q33-term	head and neck (Speicher 1995)
7	colon (Schlegel 1995); glioma (Kim), head and neck (Speicher); prostate (Visakorpi)
8q	small cell lung (Ried 1994)
8q21	bladder (Kallioniemi 1995)
8q24	myeloid leukemia (Mohamed)
8q22-24	glioma (Kim; Muleris 1994b); breast (Muleris 1994a)
8q24-25	small cell (Levin 1994; Ried 1994); breast (Muleris 1994a)
8q23-term	sarcoma (Forus 1995a), melanoma (Speicher)
8q24	ovarian (Iwabuchi)
8q	breast (Ried 1995; Isola; Muleris 1994a), small cell lung (Levin 1994 & 1995), B-cell leukemias (Bentz 1994a), myeloid leukemia (Bentz 1994b), glioma (Schlegel), head and neck (Speicher 1995), prostate (Cher, Visakorpi)
9	head and neck (Speicher)
9p	head and neck (Speicher)
9p2	glioma (Muleris 1994b)
9p13	breast (Muleris 1994a)
10p	head and neck (Speicher 1995)
10p13-14	bladder (Voorter)
10q22	breast (Muleris 1994a)
11q13	head and neck (Speicher 1995), breast (Muleris 1994a)



TABLE 12: Cancer cell lines sharing duplicated chromosomal regions	
Chromosomal location	Cancer type & references
12	B-cell leukemias (Bentz 1995a)
12p	head and neck (Speicher 1995), glioma (Schrock)
12q	glioma (Schlegel 1994)
12q12-15	bladder (Voorter), osteosarcoma (Tarkkanen), liposarcoma (Suijkerbuijk)
12q21.3-22	liposarcoma (Suijkerbuijk)
13	colon (Schlegel 1995)
13q	breast (Ried 1995), head and neck (Speicher 1995)
13q21-34	bladder (Kallioniemi 1995)
13q32-term	head and neck (Speicher 1995), small cell lung (Ried 1994)
14q	head and neck (Speicher 1995)
15q26	breast (Muleris 1994a)
16	head and neck (Speicher 1995)
16p	breast (Ried 1995)
16p11.2	breast (Muleris 1994a)
17	head and neck (Speicher 1995)
17p11-12	osteosarcoma (Forus 1995a; Tarkkanen)
17q	breast (Ried 1995), small cell lung (Ried 1994)
17q21.1	breast (Muleris 1994a)
17q22-23	bladder (Voorter), breast (Muleris 1994a)
17q22-24	breast (Kallioniemi 1994)
18p11	bladder (Voorter)
19q13.1	small cell lung (Ried 1994)
20p	head and neck (Speicher 1995)
20q	ovarian (Iwabuchi), colon (Schlegel 1995), breast (Isola; Tanner)
20q13.3	breast (Muleris 1994a), Kallioniemi (1994)
22q	head and neck (Speicher 1995)
22q11-13	bladder (Voorter), glioma (Schrock)
X	prostate (Visakorpi)
Xq	small cell lung (Levin 1995)
Xq24	small cell (Levin 1994)
Xq11-13	prostate (Visakorpi), osteosarcoma (Tarkkanen)

Control RNA is prepared from normal tissues to match that of the cancer cells in the experiment. Normal tissue is obtained from autopsy, biopsy, or surgical resection. Absence of neoplastic cells in the control tissue is confirmed, if necessary, by standard histological techniques.

5 cDNA corresponding to RNA that is overabundant in cancer cells and duplicated in a proportion of

the same cells is characterized further, as in Examples 3-7. Additional cDNA comprising an entire protein-product encoding region is rescued or selected according to standard molecular biology techniques as described elsewhere in this disclosure.

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TABLE OF SEQUENCE LISTINGS:

10

SEQ ID NO	Designation	Description	Type	
1	CH1-9a11-2	152 bp sequence (fragment)	dsDNA	Figure 22
2		translation	amino acid	Figure 22
3	CH8-2a13-1	163 bp sequence (fragment)	dsDNA	Figure 22
4		translation	amino acid	Figure 22
5	CH13-2a12-1	107 bp sequence (fragment)	dsDNA	Figure 22
6		translation	amino acid	Figure 22
7	CH14-2a16-1	114 bp sequence (fragment)	dsDNA	Figure 22
8		translation	amino acid	Figure 22
9 to 14	Primers		ssDNA	Table 2
15	CH1-9a11-2	3.5 kb nucleotide sequence	dsDNA	Figure 8
16		translation	amino acid	Figure 9
17		protein	amino acid	Figure 9
18	CH8-2a13-1	4.0 kb nucleotide sequence	dsDNA	Figure 11
19		translation	amino acid	Figure 12
20		protein	amino acid	Figure 12
21		4.1 kb sequence (predicted)	dsDNA	Figure 13
22		translation	amino acid	Figure 14
23	CH13-2a12-1	3.3 kb nucleotide sequence	dsDNA	Figure 16
24		translation	amino acid	Figure 17
25		protein	amino acid	Figure 17
26	CH14-2a16-1	2.0 kb nucleotide sequence	dsDNA	Figure 19
27		translation	amino acid	Figure 20
28		protein	amino acid	Figure 20
29		0.6 kb nucleotide sequence	ssDNA	Figure 21
30		translation	amino acid	Figure 21

SEQ. ID NO	Designation	Description	Type	
31		0.3 kb nucleotide sequence	ssDNA	Figure 21
32		translation	amino acid	Figure 21
33	CH1-9a11-2	3.5 kb nucleotide sequence	dsDNA	Figure 23
34		translation	amino acid	Figure 24
35	CH14-2a16-1	2.0 kb nucleotide sequence	dsDNA	Figure 25
36		translation	amino acid	Figure 26
37		protein	amino acid	Figure 26
38 & 39	Motif	Zinc-finger binding domain	dsDNA	text
40-43	Primers		ssDNA	text
44 & up	Primers		ssDNA	Figures 7, 10, 15, 18

5	SEQ ID NO:9: TTTTTTTTT TCC	13
	SEQ ID NO:10: TTTTTTTTT TAC	13
10	SEQ ID NO:11: CAATCGCCGT	10
	SEQ ID NO:12: TCGGCGATAG	10
15	SEQ ID NO:13: CAGCACCCAC	10
20	SEQ ID NO:14: AGCCAGCGAA	10



CLAIMS

What is claimed as the invention is:

- 5       1. An isolated polynucleotide comprising a linear sequence of at least 10 nucleotides identical to a linear sequence contained in a polynucleotide selected from the group consisting of CH8-2a13-1, CH13-2a12-1, CH14-2a16-1, and CH1-9a11-2.
- 10       2. An isolated polynucleotide comprising a linear sequence of at least 40 consecutive nucleotides at least 90% identical to a linear sequence contained in a sequence selected from the group consisting of SEQ. ID NO:15, SEQ. ID NO:18, SEQ. ID NO:21, SEQ. ID NO:23, SEQ. ID NO:26, SEQ. ID NO:29, SEQ. ID NO:31, SEQ. ID NO:33, and SEQ. ID NO:35; but not in any of SEQ. ID NOS: 1, 3, 5, and 7.
- 15       3. The isolated polynucleotide of claim 2, comprising a linear sequence of at least 100 consecutive nucleotides at least 90% identical to a sequence contained in the selected sequence.
- 20       4. The isolated polynucleotide of claim 2, comprising a linear sequence of at least 40 consecutive nucleotides at least 95% identical to a sequence contained in the selected sequence.
- 25       5. An isolated polynucleotide comprising a linear sequence of at least 40 consecutive nucleotides that hybridizes with a DNA having a sequence selected from the group consisting of SEQ. ID NO:15, SEQ. ID NO:18, SEQ. ID NO:21, SEQ. ID NO:23, SEQ. ID NO:26, SEQ. ID NO:29, SEQ. ID NO:31, SEQ. ID NO:33, and SEQ. ID NO:35; under conditions where it does not hybridize with SEQ. ID NOS: 1, 3, 5, 7, or any other DNA from a human cell.
- 30       6. The isolated polynucleotide of claim 5, wherein the linear sequence is at least 100 consecutive nucleotides
- 35       7. An isolated polynucleotide comprising a sequence of at least 40 consecutive nucleotides that hybridizes with an RNA having a sequence selected from the group consisting of SEQ. ID NO:15, SEQ. ID NO:18, SEQ. ID NO:21, SEQ. ID NO:23, SEQ. ID NO:26, SEQ. ID NO:29, SEQ. ID NO:31, SEQ. ID NO:33, and SEQ. ID NO:35; under conditions where it does not hybridize with SEQ. ID NOS: 1, 3, 5, 7, or any other RNA from a human cell.

8. The isolated polynucleotide of claim 7, wherein the linear sequence is at least 100 consecutive nucleotides
- 5 9. The isolated polynucleotide of any of claims 2-8, wherein said linear sequence is contained in a duplicated gene or overabundant RNA in cancerous cells.
- 10 10. The isolated polynucleotide of any of claims 2-8, which is a CH13-2a12-1 polynucleotide, and is contained in an encoding region for a protein or RNA molecule that controls cell proliferation.
- 11 11. The isolated polynucleotide of any of claims 2-8, which is a CH14-2a16-1 polynucleotide, and is contained in an encoding region for a protein with DNA or RNA binding activity.
- 15 12. The isolated polynucleotide of any of claims 2-8, present in a recombinant plasmid deposited under ATCC Accession No. 98074
- 13 13. The isolated polynucleotide of any of claims 2-8, present in a recombinant phage deposited under ATCC Accession No. 97595.
- 20 14. The isolated polynucleotide of any of claims 2-8, present in the  $\lambda$ BCBT474 cDNA library deposited under ATCC Accession No. 97594.
- 25 15. An isolated polynucleotide comprising a linear sequence of polynucleotides essentially identical to a sequence selected from the group consisting of SEQ. ID NO:15, SEQ. ID NO:18, SEQ. ID NO:21, SEQ. ID NO:23, SEQ. ID NO:26, SEQ. ID NO:29, SEQ. ID NO:31, SEQ. ID NO:33, and SEQ. ID NO:35.
- 30 16. An isolated polypeptide comprising a linear sequence of at least 5 amino acid residues identical to a sequence encoded by a polynucleotide selected from the group consisting of CH1-9a11-2, CH8-2a13-1, CH13-2a12-1, and CH14-2a16-1.
- 35 17. An isolated polypeptide comprising a linear sequence of at least 5 consecutive amino acids identical to a linear sequence contained in a sequence selected from the group consisting of SEQ. ID NO:17, SEQ. ID NO:20, SEQ. ID NO:22, SEQ. ID NO:24, SEQ. ID NO:28, SEQ. ID NO:30, SEQ. ID NO:32, SEQ. ID NO:34, and SEQ. ID NO:37; but not in any of SEQ. ID NOS: 2, 4, 6, and 8.
18. The isolated polypeptide of claim 17, comprising a linear sequence of at least 15 consecutive amino acids at least 90% identical to a linear sequence contained in the selected sequence.

19. The isolated polypeptide of claim 17 or 18, wherein said linear sequence is encoded in a duplicated gene or overabundant RNA in cancerous cells.
- 5 20. The isolated polypeptide of claim 17 or 18, which is overexpressed in cancerous cells.
21. The isolated polypeptide of claim 17 or 18, wherein the polynucleotide selected from said group is a CH1-9a11-2 polynucleotide, and the polypeptide is a transmembrane polypeptide.
- 10 22. An isolated polypeptide comprising a linear sequence of amino acids essentially identical to a sequence selected from the group consisting of SEQ. ID NO:17, SEQ. ID NO:20, SEQ. ID NO:22, SEQ. ID NO:24, SEQ. ID NO:28, SEQ. ID NO:30, SEQ. ID NO:32, SEQ. ID NO:34, and SEQ. ID NO:37; but not in any of SEQ. ID NOS: 2, 4, 6, and 8.
- 15 23. An isolated polynucleotide comprising an encoding sequence for the polypeptide of any of claims 17 to 22.
24. A monoclonal or isolated polyclonal antibody specific for the polypeptide of claim 22.
- 20 25. A method of detecting gene duplication in cancerous cells, comprising the steps of:
- a) reacting DNA contained in a clinical sample with a reagent comprising the polynucleotide of claims 2-8, said clinical sample having been obtained from an individual suspected of having cancerous cells; and
- 25 b) comparing the amount of any complexes formed between the reagent and the DNA in the clinical sample with the amount of any complexes formed between the reagent and DNA in a control sample.
26. A method of detecting overabundance of RNA in cancerous cells, comprising the steps of:
- a) reacting RNA contained in a clinical sample with a reagent comprising the polynucleotide of claim 2-8, said clinical sample having been obtained from an individual suspected of having cancerous cells; and
- 30 b) comparing the amount of any complexes formed between the reagent and the RNA in the clinical sample with the amount of any complexes formed between the reagent and RNA in a control sample.

27. A method of determining gene duplication or overabundance of RNA in cancerous cells, comprising the steps of:
- 5           a) amplifying DNA or RNA in a clinical sample with a primer comprising the polynucleotide of claim 2-8 to yield an amplified polynucleotide, said clinical sample having been obtained from an individual suspected of having cancerous cells; and
- b) comparing the amount of polynucleotide amplified from the DNA or RNA with the amount of polynucleotide amplified from DNA or RNA from a control sample.
- 10   28. A method of screening for cancer associated with a gene duplication in an individual, comprising the steps of:
- a) determining gene duplication in cells from the individual according to the method of claim 25; and
- 15           b) correlating any gene duplication determined in step a) with an increased risk for the cancer.
29. A method of screening for cancer associated with overexpression of RNA in an individual, comprising the steps of:
- 20           a) determining overexpression of RNA in cells from the individual according to the method of claim 26; and
- b) correlating any RNA overexpression determined in step a) with an increased risk for the cancer.
- 25   30. A method of screening for cancer associated with a gene duplication or overexpression of RNA in an individual, comprising the steps of:
- a) determining gene duplication or overexpression of RNA in cells from the individual according to the method of claim 27; and
- b) correlating any gene duplication or overexpression of RNA determined in step a) with an increased risk for the cancer.

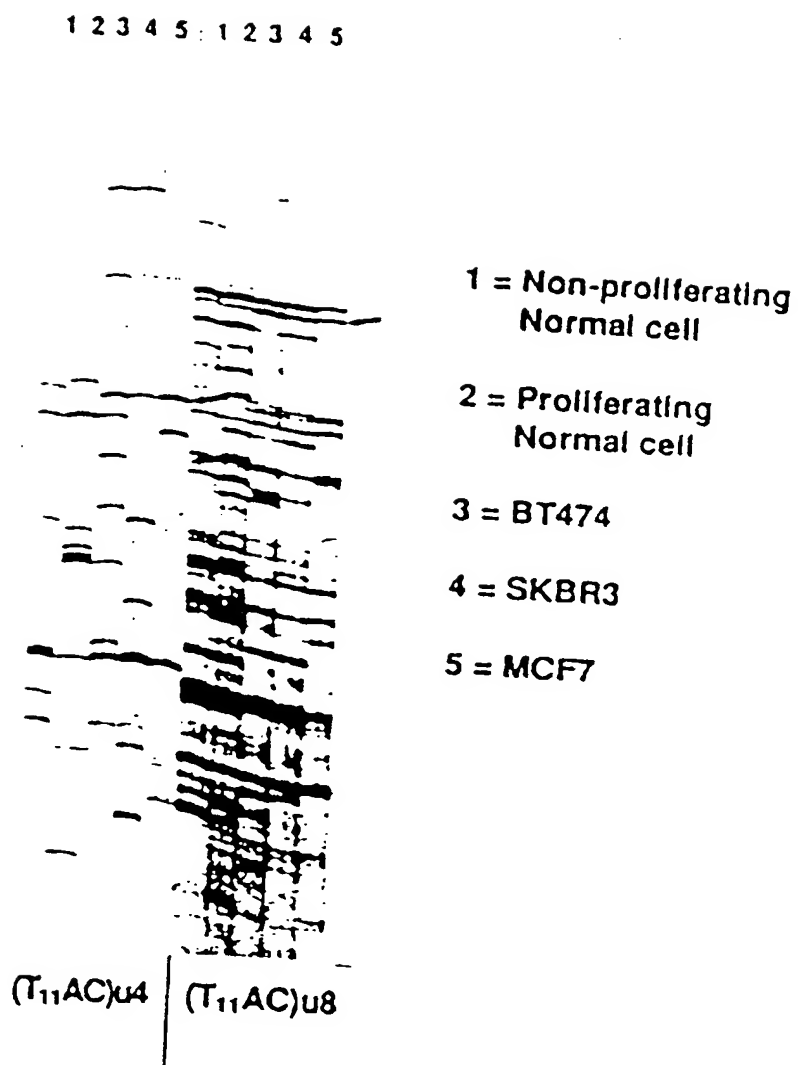
31. The method of any of claims 28-30, which is a screening method for breast cancer.
32. A diagnostic kit for detecting gene duplication or RNA overabundance in cells contained in an individual as manifest in a clinical sample, comprising a reagent and a buffer in suitable packaging, wherein the reagent comprises the polynucleotide of any of claims 2-8.
33. A method for detecting altered protein expression in cancerous cells, comprising the steps of:
- reacting a polypeptide contained in a clinical sample with a reagent comprising the antibody of claim 24, said clinical sample having been obtained from an individual suspected of having cancerous cells; and
  - comparing the amount of any complexes formed between the reagent and the polypeptide in the clinical sample with the amount of any complexes formed between the reagent and a polypeptide in a control sample.
34. A diagnostic kit for detecting a polypeptide present in a clinical sample, comprising a reagent and a buffer in suitable packaging, wherein the reagent comprises the antibody of claim 24.
35. A host cell genetically altered by the polynucleotide of any of claims 2 to 8 or claim 23.
36. A method of screening a pharmaceutical candidate, comprising the steps of:
- separating progeny of the cell of claim 35 into a first group and a second group;
  - treating the first group of cells with the pharmaceutical candidate;
  - not treating the second group of cells with the pharmaceutical candidate; and
  - comparing the phenotype of the treated cells with that of the untreated cells.
37. A pharmaceutical preparation for use in cancer therapy, comprising the polynucleotide of claim 2 to 8 or claim 23, said preparation being capable of reducing the pathology of cancerous cells.
38. A method for treating an individual bearing cancerous cells, comprising administering the pharmaceutical preparation of claim 37.
39. A pharmaceutical preparation for use in cancer therapy, comprising the antibody of claim 24, said preparation being capable of reducing the pathology of cancerous cells.
40. A method for treating an individual bearing cancerous cells, comprising administering the pharmaceutical preparation of claim 39.

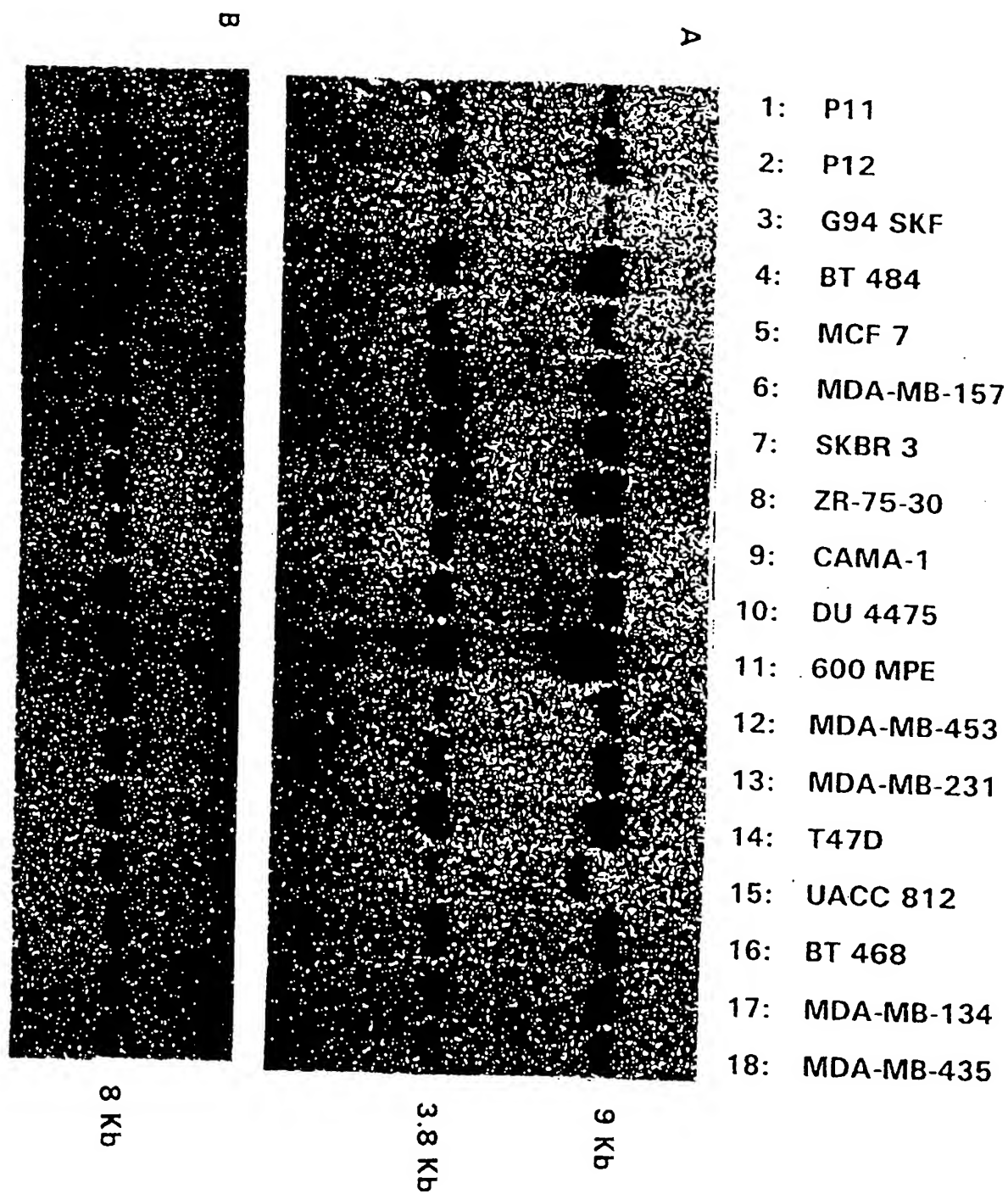
41. A pharmaceutical preparation comprising the polypeptide of claim 17 or 18 in an immunogenic form, and a pharmaceutically compatible excipient.
- 5 42. A method for treatment of cancer, comprising administration of the pharmaceutical preparation of claim 41.
43. A method for obtaining cDNA corresponding to a gene that is duplicated or overexpressed in cancer, comprising the steps of:
- 10 a) supplying an RNA preparation from control cells;
- b) supplying RNA preparations from at least two different cancer cells;
- c) displaying cDNA corresponding to the RNA preparations of step a) and step b) such that different cDNA corresponding to different RNA in each preparation are displayed separately;
- 15 d) selecting cDNA corresponding to RNA that is present in greater abundance in the cancer cells of step b) relative to the control cells of step a);
- e) supplying a digested DNA preparation from control cells;
- f) supplying digested DNA preparations from at least two different cancer cells;
- 20 g) hybridizing the cDNA of step d) with the digested DNA preparations of step e) and step f); and
- h) further selecting cDNA from the cDNA of step d) corresponding to a gene that is duplicated in the cancer cells of step f) relative to the control cells of step e).
44. The method of claim 43, wherein the two different cancer cells used to supply RNA in step b) share a duplicated gene in the same region of a chromosome.
- 25 45. The method of claim 43, wherein RNA preparations from at least three different cancer cells are supplied in step b).
- 30 46. The method of claim 43, wherein the three different cancer cells used to supply RNA in step b) share a duplicated gene in the same region of a chromosome.
47. The method of claim 43, wherein the control cells of step a) are uncultured.
- 35 48. The method of claim 43, further comprising supplying a digested mitochondrial DNA preparation; hybridizing the cDNA of step h) with the digested mitochondrial DNA preparation; and further selecting cDNA from the cDNA of step h) corresponding to genes that do not hybridize with the digested mitochondrial DNA preparation.

49. The method of claim 43, further comprising the steps of:
- i) supplying an RNA preparation from control cells;
  - j) supplying RNA preparations from at least two different cancer cells;
  - k) hybridizing the cDNA of step h) with the RNA preparations of step i) and step j); and
  - l) further selecting cDNA from the cDNA of step h) corresponding to RNA that is present in greater abundance in the cancer cells of step j) relative to the control cells of step i).
50. The method of claim 49, wherein the gene to which the cDNA corresponds is not duplicated in at least one of the cancer cells used to supply the RNA in step j) relative to the control cells of step e).
51. The method of claim 43, wherein the two different cancer cells used to supply the RNA preparations in step b) are breast cancer cells.
52. The method of claim 43, wherein the two different cancer cells used to supply the RNA preparations in step b) are from a common type of cancer, wherein the type of cancer is selected from the group consisting of lung cancer, glioblastoma, pancreatic cancer, colon cancer, prostate cancer, hepatoma, and myeloma.
53. The method of claim 43, wherein the two different cancer cells used to supply the digested DNA preparations in step f) are breast cancer cells.
54. The method of claim 43, wherein the two different cancer cells the digested DNA preparations in step f) are from a common type of cancer, wherein the type of cancer is selected from the group consisting of lung cancer, glioblastoma, pancreatic cancer, colon cancer, prostate cancer, hepatoma, and myeloma.
55. A method for obtaining cDNA corresponding to a gene that is deleted or underexpressed in cancer, comprising the steps of:
- a) supplying an RNA preparation from control cells;
  - b) supplying RNA preparations from at least two different cancer cells that share a deleted gene in the same region of a chromosome;
  - c) displaying cDNA corresponding to the RNA preparations of step a) and step b) such that different cDNA corresponding to different RNA in each preparation are displayed separately; and
  - d) selecting cDNA corresponding to RNA that is present in lower abundance in the cancer cells of step b) relative to the control cells of step a).

56. The method of claim 55, further comprising the steps of:
- e) supplying a digested DNA preparation from control cells;
  - f) supplying digested DNA preparations from at least two different cancer cells;
  - 5 g) hybridizing the cDNA of step d) with the digested DNA preparations of step e) and step f); and
  - h) further selecting cDNA from the cDNA of step d) corresponding to a gene that is deleted in the cancer cells of step f) relative to the control cells of step e).
- 10 57. A method for characterizing a gene that is duplicated or has altered expression in cancer, comprising obtaining cDNA corresponding to the gene according to the method of any of claims 43-56, and then sequencing the cDNA.
- 15 58. A method of screening a candidate drug for cancer treatment, comprising obtaining cDNA corresponding to a gene that is duplicated or has altered expression in cancer according to the method of any of claims 43-56, and comparing the effect of the candidate drug on a cell genetically altered with the cDNA with the effect on a cell not genetically altered with the cDNA.



**Figure 1**

**Figure 2**

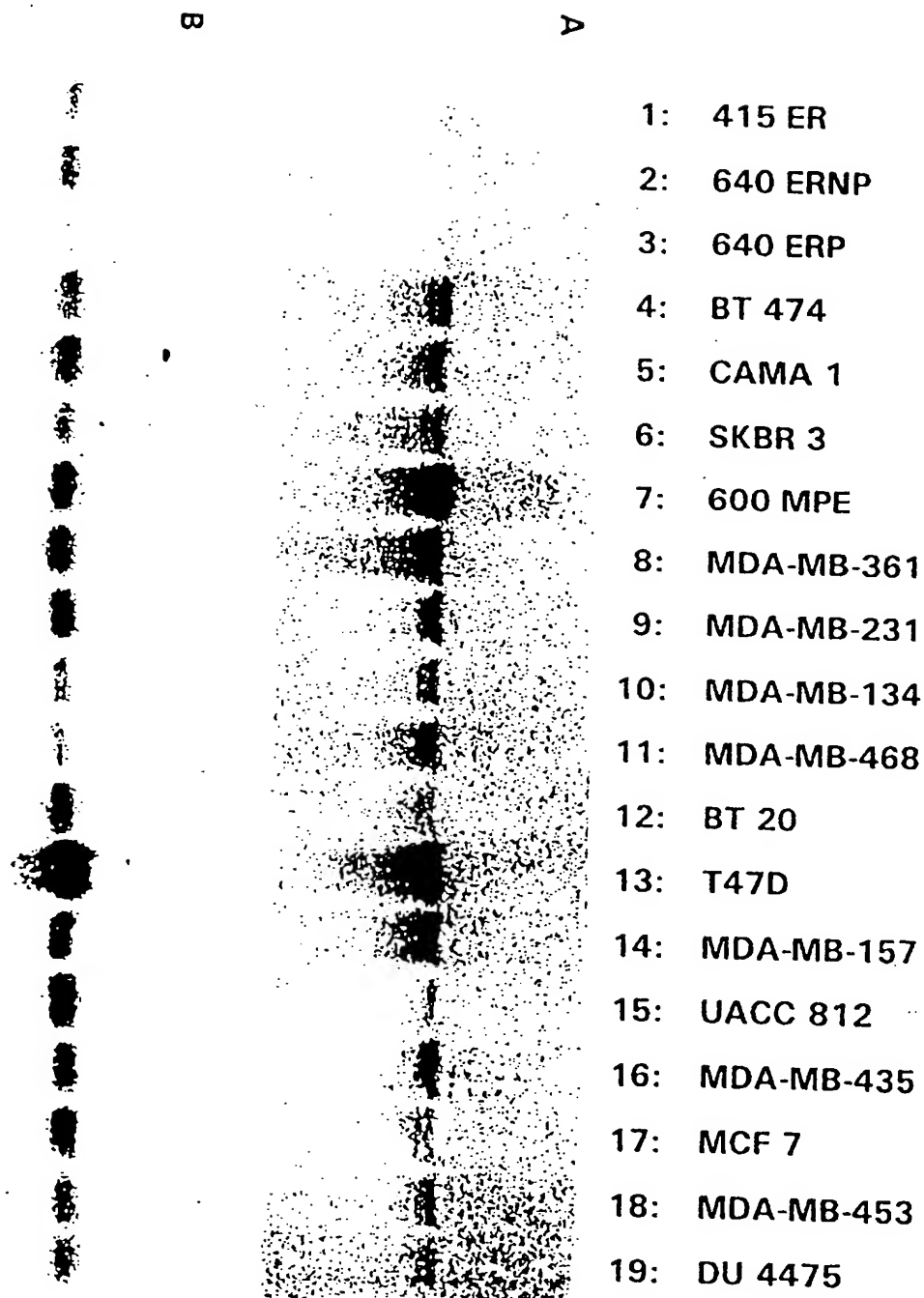
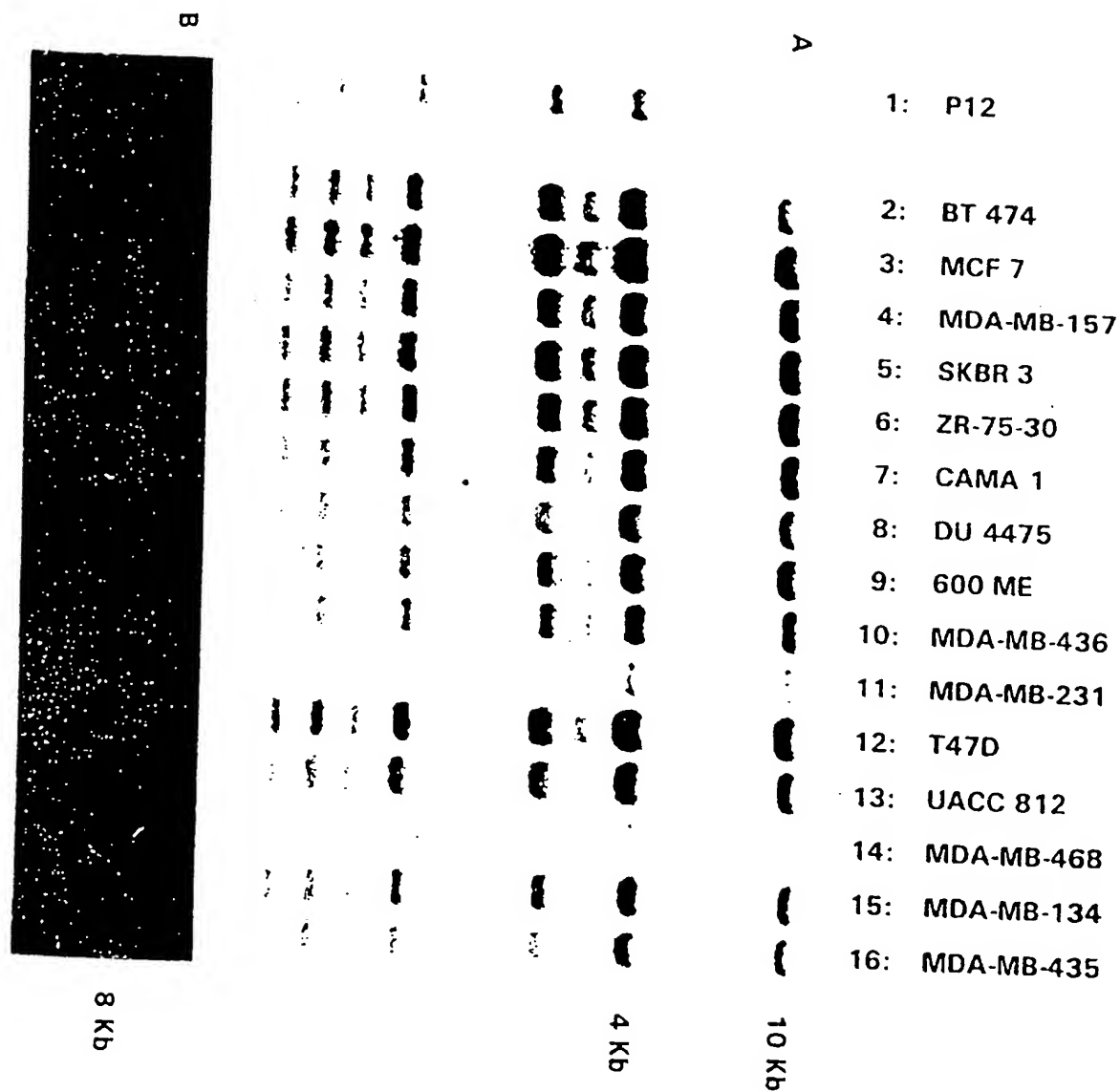
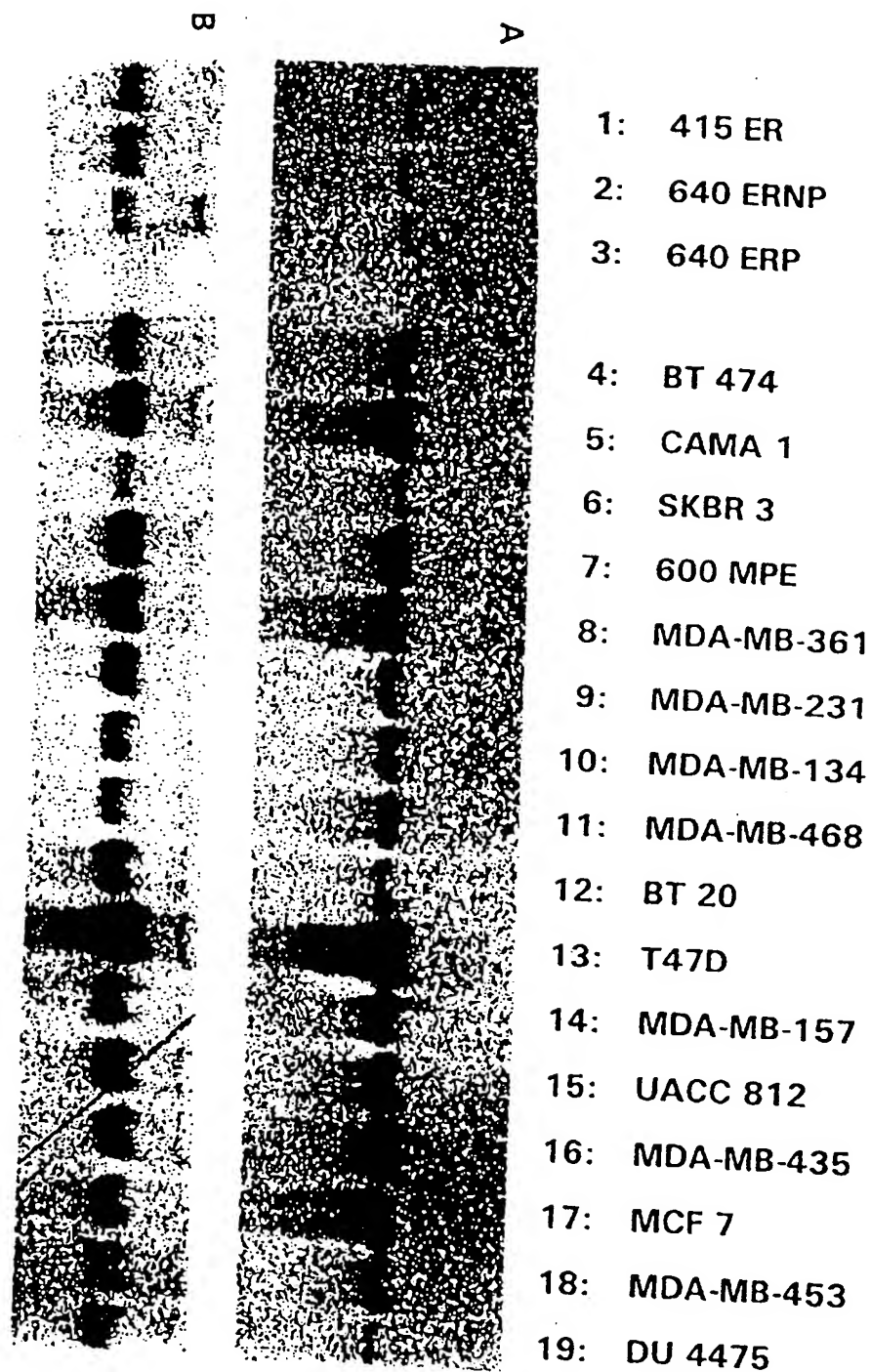
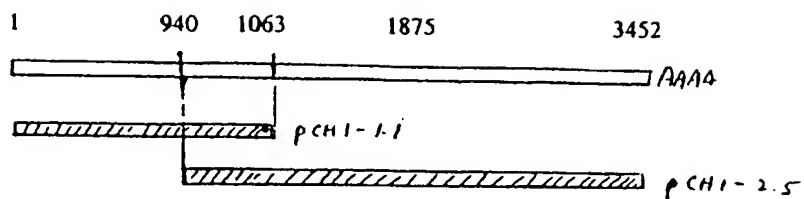
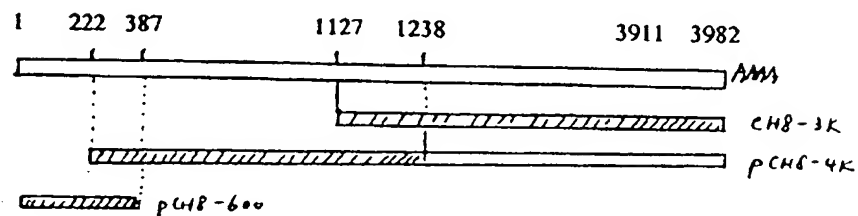
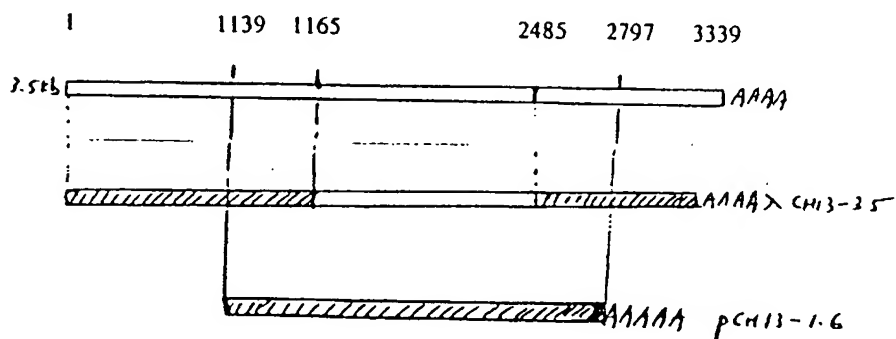
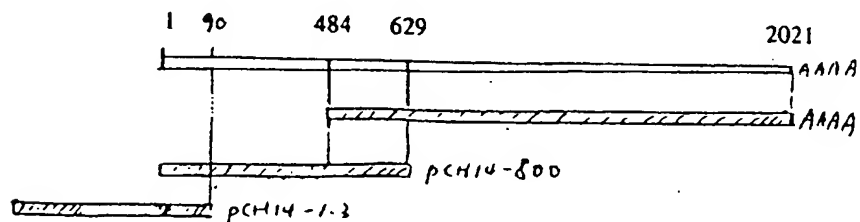
**Figure 3**

Figure 4



**Figure 5**

**Figure 6****CH1-9a11-2****CH8-2a13-1****CH13-2a12-1****CH14-2a16-1**

**Figure 7**

<b>+ strand (sense)</b>		<b>sequence (5'--&gt;3')</b>
	1st base	
1. pchl-t7-1f	1123	CGG GAG GTT TCA GAT CGA C
2. pchl-t7-2f	1437	GCG CTG CAA GTA CAA AAT TG
3. pchl-t7-3f	1729	TCT AAA GTC CAA GAC CAA GG
4. pchl-t7-4f	1987	CAG AAA TTA TGG TTT CTA CC
5. pchl-t7-5f	2266	CaG GAA GAG GAG GGA TAA C
6. pchl-sp6-3fb	2684	(T) AAA CAT ACA CAA TAA ACA C
7. pchl-sp6-2rb	2966	TTG GCA GCG ACT GTA TTT G
8. pchl-sp6-1rb	3283	CCT GAT TTT ATA GAA GCC CC
<b>- strand (antisense)</b>		
9. pchl-sp6-1f	3302	GGG GCT TCT ATA AAA TCA GG
10. pchl-sp6-2f	2987	ATT CAA ATA CAG TTG CTG C
11. pchl-sp6-3f	2705	TTA GTG TTT ATT GTG TAT G
12. pchl-sp6-4f	2458	AGT GTT CAT TTC CAG TGA G
13. pchl-sp6-5f	2066	CTT TGT TCT TGG ACT TTA G
14. pchl-t7-3fb	1748	CCT TGG TCT TGG ACT TTA G
15. pchl-t7-2rb	1445	AAT TTT GTA CTT GCA GCG C
16. pchl-t7-1rb	1141	GTC GAT CTG AAA CCT CCC G
17. CH1a	1063	GTG CCT GTA GCA ACT GGA TGG C
18. CH1b	1079	GTC ATG TTG GTC AGC TGT GCC

**Figure 8(A)**

1	GAATACATAT	ATAAATGGTG	TTCAGTTAGA	GTTGCTCTTT	ATCGGCAGCG
51	CAGCCGAAC	GCTTTGAGTA	AAGGAAAAGA	TTATCTTGTG	TTAGCTCAAC
101	CACCCTTACT	ACTTCCTGCG	GAATCAGTAG	ATGTTTCAGT	ATIGCAACCT
151	CTGAGTGGAG	AATTGGAAAA	TACGAATATA	GAAAGGGAAG	CTGAAACTGT
201	TGTTCTGGGT	GATTTAAGTA	GTAGTATGCA	CCAGGATGAC	TTGGTGAATC
251	ACACTGTAGA	TGCAGTTGAA	CTTGAACCAA	GCCATTCTCA	AACTCTTTCT
301	CAGTCTCTTC	TTTTAGATAT	TACCCAGAA	ATCAATCCCT	TGCCTAAAAAT
351	AGAAGTATCT	GAGTCTGTTG	AATATGAGGC	AGGACATATA	CCATCACCAG
401	TGATTCCCCA	AGAGAGTTCT	GTTGAGATCG	ATAATGAAAC	AGAACAAAAG
451	TCTGAGAGCT	TTAGTTCTAT	AGAGAAACCA	TCTATTACCT	ATGAAACAAA
501	TAAAGTTAAT	GAGTTAAATG	ATAATATTAT	AAAAGAAGAT	ATGAACTCCA
551	TGCAAAATTT	CACAAAGCTG	TCTGAAACAA	TAGTGCCACC	AATAAATACA
601	GCCACTGTAC	CCGACAATGA	AGATGGGGAA	GCCAAAATGA	ATATAGCTGA
651	CACAGCAAAG	CAAACCTTGA	TTTCTGTTGT	GGATTCTTCT	TCATTACCTG
701	AAGTAAAAGA	AGAAGAACAG	TCTCCAGAAG	ATGCCCTTTT	GAGAGGGTTA
751	CAGAGGACAG	CTACAGATTT	TTATGCTGAA	TTGCAAAATT	CTACAGATCT
801	AGGATATGCT	AATGGAAATC	TTGTACATGG	ATCAAACCAA	AAGGAGTCAG
851	TATTTATGAG	ACTTAATAAT	CGTATTAAAG	CCTTAGAAGT	TAACATGTCT
901	CTCAGTGGTC	GCTATCTGGA	GGAGCTTAGC	CAAAGGTACC	GAAAACAAAT
951	GGAAGAAATG	CAAAGGCTT	TCAACAAAAC	AATCGTGAAA	CTTCAGAAAT
1001	CTTCAAGAAT	AGCAGAGGAG	CAGGATCAGC	GGCAAACTGA	AGCCATCCAG
1051	TTGCTACAGG	CACAGCTGAC	CAACATGACA	CAGCTTGTCT	CAAATTTATC
1101	AGCAACAGTA	GCAGAAATGA	AACGGGAGGT	TTCAGATCGA	CAAAGCTATC
1151	TTGTCATATC	TTTGGTTCTT	TGTGTGTCT	TGGGACTGAT	GCTTTGTATG
1201	CAGCGTTGTC	GAAATACTTC	TCAATTTGAT	GGAGATTATA	TTTCAAAACT
1251	TCCTAAAAAGT	AATCAGTATC	CAAGCCCTAA	AAGGTGTTTC	TCTTCCTATG
1301	ATGATATGAA	TTTGAAGAAG	AGAACTTCAT	TCCCACTCAT	GAGATCCAAG
1351	TCTCTACAGT	TAACGTGCAA	AGAAAGTAGC	CCAAATGATT	TGTACATTGT
1401	AGAACCCCTC	AAGTTTTCTC	CAGAAAAGAA	GAAGAAGCGC	TGCAAGTACA
1451	AAATTGAAAA	AATTGAGACC	ATAAAGCCTG	AAGAACCATT	GCACCCCAT
1501	GCCAATGGCG	ACATAAAAGG	AAGAAAGCCC	TTTACGAACC	AGAGAGATTT
1551	TTCTAATATG	GGAGAAGTTT	ATCACTCTTC	TTATAAAGGT	CCTTCCATCG
1601	AAGGAAGCTC	AGAACTTCA	TCACAGTCAG	AAGAGTCCTA	TTTTTGTGGC
1651	ATTTTCAGCTT	GCACAAGTCT	GTGCAATGGA	CAGTCTCAAA	AGACAAAAAC
1701	TGAGAAGAGG	GCTTTAAAAC	GAAGACGATC	TAAAGTCCAA	GACCAAGGAA
1751	AATIGATAAA	AACTCTAATA	CAGACTAAGT	CGGGATCATT	GCCGAGCCTG
1801	CATGACATAA	TCAAAGGAAA	CAAAGAGATC	ACCGTGGGAA	CATTTGGTGT
1851	TACAGCAGTC	TCGGGACATA	TCTAAAATTA	ATTGAACTTT	TCATACAGAA
1901	GACTTTTTTG	TTGTTGTCT	TTGAAGAACA	GTCTGTAGTA	TTTGAAGGGT
1951	TTGGGGGAGG	GAGAAAATAT	TAATGGGAAA	GGCATTCAGA	AATTATGGTT
2001	TCTACCTTTT	TAAAAAGTAG	ATGGGATTGT	GCTCAATCTT	GGTTAATGAG
2051	CTACAGTTTT	ACAAAGCTGA	TCACTTCCTA	TAAGGACAAT	GGTAGACATT
2101	TTATAAAGAT	GTTTTTTCAC	AAGATTAAAT	ACTGGGACAA	AAGTAATTTG
2151	GAAGCCAGT	TCCTTAGGTG	GGATAGGAAT	GAAAGCCTAA	ACCTCTTCCT
2201	TTAGCTTTGT	TCCTATTTCT	TGCACCTTCC	CATATTTATG	TGCTTTTGT
2251	CTATTTATAA	TGCCACTGGA	AGAGGAGGGA	TAACTTTTTC	TGTTATTTGA
2301	TTTCTTTTAT	AACCTTGTGA	GGTTTTTGAA	GCTGCAACA	CTACAATGCT
2351	TTGAGGGGGT	CTGTGCCTGA	AGCTCAGGAG	TGTGGATCAG	ACAGTCTAAA
2401	GATCCTAAAA	ACTTGCCAAC	TGGATCTTTG	TTTAGCAAAC	TCACTGGAAA
2451	TGAACACTTA	ATGGAATTTT	TAAGTCIGTT	CTGTTAGGTA	GATGGTGAATG
2501	CTCTTGTTAT	TTTCACTTAT	TCAGGCTGGA	TFACTTCTTA	CTTAGTTACT
2551	AACTCAATGA	GGAAAAATC	CCTACAGGAT	CTTTTTTTGC	AAACAACCTGA



**Figure 8(B)**

2601	TATATGCAGA	CAAATTTTGT	ACAAATTCAC	CTTTTAAACA	CGACGTTAAC
2651	CGATTTGTGA	AGGTTTTCTT	TAGCTTACAT	TTTAAACATA	CACAAATAAAC
2701	ACTAATCCTC	CAAACCTTCA	CTGTTTTTAT	TAGTATGAAT	ATAAAATTTG
2751	AAGGTTTGGC	CAATTAGTAC	AAGTCTCATG	ATATAATCAC	AGCCTGCATA
2801	CATATGCACA	GATCCAGTTA	GTGAGTTTGT	CAAGCTTAAT	CTAATTGGTT
2851	AAGTCTAAAG	AGATTATTAT	TCCTTGATGT	TTGCTTTGTA	TTGGCTACAA
2901	ATGTGCAGAG	GTAATACATA	TGTGATGTCG	ATGTCTCTGT	CTTTTMTTTT
2951	GTCTTTAAAA	AATAATTGGC	AGCAACTGTA	TTTGAATAAA	ATGATTTCCTT
3001	AGTATGATTG	TACAGTAATG	AATGAAAGTG	GAACATGTTT	CTTTTGTAAA
3051	GGGAGAGAAT	TGACCATTTA	TTGTTGTGAT	GTTTAAGTTA	TAACTTATTG
3101	AGCACTTTTA	GTAGTGATAA	CTGTTTTTAA	ACTTGCCTAA	TACCTTTCTT
3151	GGGTATTGTT	TGTAATGTGA	CTTATTTAAC	GCCTTCTTTG	TTTGTTTAAG
3201	TTGCTGCTTT	AGGTTAACAG	CGTGTTTTAG	AAGATTTAAA	TTTCTTTCCT
3251	GTCTGCACAA	TTAGCTATTG	AGAGCAAGAG	GGCCTGATTT	TATAGAAGCC
3301	CCTTGAAAAG	AGGTCCAGAT	GAGAGCAGAG	ATACAGTGAG	AAATTATGTG
3351	ATCTGTGTGT	TGTGGGAAGA	GAATTTTCAA	TATGTAACATA	CGGAGCTGTA
3401	GTGCCATTAG	AAACTGTGAA	TTTCCAAATA	AATCTGAACA	CTTGTCTTTA
3451	TT				

**Figure 9**

1	EYIYKWCVR	VALYRQRSRT	ALSKGKDYL	LAQPPLLLPA	ESVDVSVLQP
51	LSGELENTNI	EREAEVVLG	DLSSSMHQDD	LVNHTVDAVE	LEPSHSQTLS
101	QSLLLDITPE	INPLPKIEVS	ESVEYEAGHI	PSPVIPQESS	VEIDNETEQK
151	SESFSSIEKP	SITYETNKVN	ELMDNIIKED	MNSMQIFTKL	SETIVPPINT
201	ATVPDNEDGE	AKMNIADTAK	QTLISVVDSS	SLPEVKEEEQ	SPEDALLRGL
251	QRTATDFYAE	LQNSTDLGYA	NGNLVHGSNQ	KESVFMRLNN	RIKALEVNMS
301	LSGRYLEELS	QRYRKQMEEM	QKAFNKTIVK	LQNTSRJAE	QDQRQTEAIQ
351	LLQAQLTNMT	QLVSNLSATV	AELKREVSDR	QSYLVISLVL	CVVLGLMLCM
401	QRCRNTSQFD	GDYISKLPKS	NQYPSPKRCF	SSYDDMNLKR	RTSFPLMRSK
451	SLQLTGKEVD	PNDLYIVEPL	KFSPEKKKKR	CKYKIEKIET	IKPEEPLHPI
501	ANGDIKGRKP	FTNQDQFSNM	GEVYHSSYKG	PPSEGSSETS	SQSEESYFCG
551	ISACTSLCNG	QSQKTKTEKR	ALKRRRSKVQ	DQGKLIKTLI	QTKSGSLPSL
601	HDIKGNKEI	TVGTFGVTAV	SGHI·N·LNF	SYRRLFCCCS	LKNSL·YLKG
651	LGEGENINGK	GIQKLWFLPF	·KVDGIVLNL	G··ATVLQS·	SLPIRTMVDI
701	L·RCFFTRLI	TGTRKVIWPS	SLGGIGMKA·	TSSFSFVPI	CTFPYLCAFC
751	LFIMPLEEEG	·LFLFLDFFY	NFVRFLKLQT	LQCFEGVCA·	SSGVWIRQSK
801	DPKNLPTGSL	FSKLTGNEHL	MEFLSLFC·V	DGDALVIFTY	SGWITSYLV
851	NSMRKSLQD	LFLQTTDICR	QIFDKFTF·T	RR·PICEGFL	·LTF·TYTIN
901	TNPPNFHCFY	·YEYKI·RFG	QLVQVS·YNH	SLHTYAIQI	VSLSSLI·LV
951	KSKEIIP·C	LLCIGYKCAE	VIHM·CRCLC	LFFCL·KIIG	SNCI·IK·FL
1001	SMIVQ··MKV	EHVSF·KGEN	·PFIVVMFKL	·LIEHF·····	LFLNLPNTFL
1051	GYCL·CDLFN	AFFVCLSCCF	RLTACFRFRK	FLSCLHN·LF	RARGPDFIEA
1101	P·KEVQMRAE	IQ·EIM·SVC	CGKRIFNM·L	RSCSAIRNCE	FPNKSEHLSL

1	EYIYKWCVR	VALYRQRSRT	ALSKGKDYL	LAQPPLLLPA	ESVDVSVLQP
51	LSGELENTNI	EREAEVVLG	DLSSSMHQDD	LVNHTVDAVE	LEPSHSQTLS
101	QSLLLDITPE	INPLPKIEVS	ESVEYEAGHI	PSPVIPQESS	VEIDNETEQK
151	SESFSSIEKP	SITYETNKVN	ELMDNIIKED	MNSMQIFTKL	SETIVPPINT
201	ATVPDNEDGE	AKMNIADTAK	QTLISVVDSS	SLPEVKEEEQ	SPEDALLRGL
251	QRTATDFYAE	LQNSTDLGYA	NGNLVHGSNQ	KESVFMRLNN	RIKALEVNMS
301	LSGRYLEELS	QRYRKQMEEM	QKAFNKTIVK	LQNTSRJAE	QDQRQTEAIQ
351	LLQAQLTNMT	QLVSNLSATV	AELKREVSDR	QSYLVISLVL	CVVLGLMLCM
401	QRCRNTSQFD	GDYISKLPKS	NQYPSPKRCF	SSYDDMNLKR	RTSFPLMRSK
451	SLQLTGKEVD	PNDLYIVEPL	KFSPEKKKKR	CKYKIEKIET	IKPEEPLHPI
501	ANGDIKGRKP	FTNQDQFSNM	GEVYHSSYKG	PPSEGSSETS	SQSEESYFCG
551	ISACTSLCNG	QSQKTKTEKR	ALKRRRSKVQ	DQGKLIKTLI	QTKSGSLPSL
601	HDIKGNKEI	TVGTFGVTAV	SGHI		

**Figure 10**

<b>+ strand (sense)</b>		sequence (5'-->3')
1. pch8-sp6-1f	369	GCT AAG CCA GAG CTA CAG G
2. pch8-sp6-2f	677	tCT GAT CTT CTG CTG ATT C (CTC)
3. pch8-1fa	1238	TCT GAA CTG CCT GAG AGA C
4. pch8-2f	1462	CCA AAT GGG AGC ATT ACA AG
5. pch8-3f	1745	TCA TCA AAT GAT CAG AAC C
6. pch8-4f	1995	ATT CTG GAG AGT TGG TAT CC
7. pch8-5f	2277	GGA ATA AGG AAA GAG CTT G
8. pch8-6f	2559	TCC ACT CAT ATT CCA ATA CC
9. pch8-5rb	2849	CCT GAG AGA CAG AAC TGT TC
10. pch8-4rb	3090	GGA CCC TTC ACT TCC TTA C
11. pch8-3rb	3370	GGC CAC CAC TTG TCC TGG G
12. pch8-2rb	3517	CAG AAC AGT GCT CTA ACT G
13. pch8-1rb	3970	GTA CTG CCT CTC TTA AAT G
<b>- strand (antisense)</b>		sequence (5'-->3')
14. pch8-2r	3617	CAG TTA CAG CAC TGT TCT G
15. pch8-3r	3360	CCC AGG ACA AGT GGT GGC C
16. pch8-4r	3140	GTA AGG AAG TGA AGG GTC C
17. pch8-5r	3849	GAA CAG TTC TGT CTC TCA GG
18. pch8-6r	3563	CTT GGG TAT TGG AAT ATG AG
19. pch8-5fb	2277	CAA GCT CTT TCC TTA TTC C
20. pch8-4fb	1999	ATA GGA TAC CAA CTC TCC AG
21. pch8-3fb	1746	TGG TTC TGA TCA TTT GAT G
22. pch8-2fb	1462	CTT GTA ATG CTC CCA TTT GG
23. pch8-1fb	1238	GTC TCT CAG GCA GTT CAG A
24. pch8-fb-1f	941	GTA GAG AAT CAC GTA CAG C
25. pch8-fb-2f	612	CAA TGA CCA GTA GCA TAA C
26. CH8-3670	3891	CAG CAT TTA AGA GAG GCA G
27. CH8a	387	CCT GTA GCT CTG GCT TAG CAT CC
28. CH8b	510	CCC CTT CAT TGA GAT CAT CTA G

Figure 11(A)

1	GTGCGCCGTG	GCGCGGCCCC	GCTGACAGGT	TCTTTAATGG	AGGAGCCAAT
51	CTCTCTGCAC	ACCTGGTTTC	ATCTAATAAT	ATACAGACAC	CAGCTCTGAG
101	GCCAGTTAAT	CATCCCCAGT	GTCCAGGCAC	AGAGTAGTCG	GTCCGCCTCA
151	CAATGTTGGA	CTTTCTAGCC	GAGAACAACC	TCTGTGGCCA	AGCAATCCTA
201	AGGATTGTTT	CCTGTGGTAA	TGCCATCATT	GCTGAACTTT	TGAGACTCTC
251	TGAGTTTATT	CCTGCTGTGT	TCAGGTAAAA	AGACAGAGCT	GATCAACAGA
301	AATATGGAGA	TATCATATTT	GATTTTCAGCT	ATTTTAAGGG	TCCAGAATTA
351	TGGGAAAGCA	AACTGGATGC	TAAGCCAGAG	CTACAGGATT	TAGATGAAGA
401	ATTTCTGTAA	AACAACATAG	AAATTGTGAC	CAGATTTTAT	TTAGCATTTT
451	AAAGTGTACA	TAAATATATT	GTAGACTTAA	ACAGATATCT	AGATGATCTC
501	AATGAAGGGG	TTTATATTCA	GCAAACCTTA	GAAACTGTGC	TTCTCAATGA
551	AGATGGAAAA	CAACTTCTAT	GTGAAGCACT	GTACTTATAT	GGAGTTATGC
601	TACTGGTCAT	TGACCAAAAG	ATTGAAGGAG	AAGTCAGAGA	GAGGATGCTG
651	GTTTCTTACT	ACCGATACAG	TGCTGCTCGA	TCTTCTGCTG	ATTCAAATAT
701	GGACGATATT	TGTAAGCTGC	TTCGAAGTAC	AGGTTATTCT	AGCCAACCAG
751	GTGCCAAAAG	ACCATCCAAC	TATCCCAGAG	GCTATTTCCA	GAGAGTGCCT
801	ATCAACGAAT	CCTTCATCAG	TATGGTCATT	GGTCGACTGA	GATCTGATGA
851	TATTTACAAC	CAGGTCTCAG	CGTATCCTTT	GCCGGAGCAT	CGCAGCACAG
901	CCCTGGCAAA	CCAAGCTGCC	ATGCTGTACG	TGATTCTCTA	CTTTGAGCCT
951	TCCATCCTTC	ACACCCATCA	AGCAAAAATG	AGAGAGATAG	TGGATAAATA
1001	CTTTCCAGAT	AATTGGGTAA	TTAGTATTTA	CATGGGGATC	ACAGTTAATC
1051	TAGTAGATGC	TTGGGAACCT	TACAAAGCTG	CAAAAACCTG	TTTAAATAAT
1101	ACCCTGGACC	TTTCAAATGT	CAGAGAACAG	GCAAGCAGAT	ATGCTACTGT
1151	CAGTGAAAGA	GTGCATGCTC	AAGTGCAGCA	ATTTCTAAAA	GAAGGTTATT
1201	TAAGGGAGGA	GATGGTTCTG	GACAAATATC	CAAAGCTTCT	GAAGTGCCTG
1251	AGAGACTGCA	ATGTTGCCAT	CCGATGGCTG	ATGCTTCATA	CAGCAGACTC
1301	AGCCTGTGAC	CCAAACAACA	AACGCCTTCG	TCAAATCAAG	GACCAGATTC
1351	TAACAGACTC	TGGGTACAAT	CCCAGGATCC	TCTTCCAGCT	GCTGTTAGAT
1401	ACTGCACAAT	TTGAGTTTAT	ACTCAAAGAG	ATGTTCAAGC	AAATGCCTTC
1451	AGAAAAGCAA	ACCAAATGGG	AGCATTACAA	GAAAGAGGGT	TCGGAGCGGA
1501	TGACTGAGCT	TGCTGATGTC	TTTTTCAGGAG	TGAAACCCCT	AACCAGAGTG
1551	GAGAAAAATG	AAAACCTTCA	AGCTTGGTTC	AGAGAGATCT	CAAAACAAAT
1601	ATTGTCTTTA	AATTATGATG	ATTCTACTGC	TGCGGGCAGA	AAAACGTATC
1651	AACTGATACA	AGCTTTGGAA	GAGGTTCAAG	AATTCCACCA	GTTGGAATCC
1701	AATCTGCAAG	TATGTCAGTT	TCTTGCCGAT	ACTCGAAAGT	TTCTTCATCA
1751	AATGATCAGA	ACCATTAACA	TTAAAGAGGA	GGTTCGTGATC	ACAATGCAGA
1801	TCGTTGGGGA	CCTTCTTTTC	GCTTGGCAGT	TGATTGACAG	TTTCACATCC
1851	ATCATGCAAG	AAAGCATAAG	GGTAAATCCA	TCCATGGTTA	CTAAACTCAG
1901	AGCTACCTTC	CTAAAGCTTG	CCTCTGCCCT	CGATCTGCCC	CTTCTTCGTA
1951	TTAATCAGGC	AAATCGCCCC	GACCTGCTCA	GCGTGTCA	GTACTATTCT
2001	GGAGAGTTGG	TATCCTATGT	GAGAAAAGTT	TTGCAGATCA	TCCCAGAAAAG
2051	CATGTTTACA	TCTCTTCTAA	AGATCATAAA	GCTTCAGACC	CACGACATTA
2101	TTGAAGTGCC	TACCCGCCTG	GACAAAGACA	AGCTGAGGGA	CTATGCTCAG
2151	CTAGGCCAC	GATACGAGGT	TGCCAAGCTT	ACTCATGCTA	TTTCCATTTT
2201	TACTGAAGGC	ATCTTAATGA	TGAAAAACGAC	TTTGGTTGGC	ATCATCAAGG
2251	TGGATCCAAA	GCAGTTGCTG	GAAGATGGAA	TAAGGAAAGA	GCTTGTGAAG
2301	CGCGTTGCCT	TTGCCCTGCA	TAGGGGACTG	ATATTCAACC	CTCGAGCCAA
2351	GCCAAGTGAA	TTGATGCCCA	AGCTGAAAGA	GTTGGGAGCG	ACCATGGATG
2401	GATTCATCG	TTCTTTTGAA	TACATACAGG	ACTATGTCAA	CATTTATGGT
2451	CTGAAGATTT	GGCAGGAAGA	AGTATCTCGT	ATCATAAATT	ACAACGTGGA
2501	GCAAGAGTGT	AATAACTTTC	TAAGAACGAA	GATTCAAGAT	TGCCAAAGCA
2551	TGTACCAGTC	CACTCATATT	CCAATACCCA	AGTTTACCCC	TGTGGATGAG

**Figure 11(B)**

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2601   TCTGTAACGT TTATTGGTCG ACTCTGCAGA GAAATCCTGC GGATCACAGA
2651   CCCAAAAATG ACATGTCACA TAGACCAGCT GAACACTTGG TATGATATGA
2701   AAACATCATCA GGAAGTGACC AGCAGCCGCC TCTTCTCAGA AATCCAGACC
2751   ACCTTGGGAA CCTTTGGTCT AAATGGCTTA GACAGGCTTC TGTGCTTTAT
2801   GATTGTAAAA GAGTTACAGA ATTTCTCTCAG TATGTTTCAG AAAATTATCC
2851   TGAGAGACAG AACTGTTTCAG GACACTTTAA AAACCCTCAT GAATGCTGTC
2901   AGTCCCCTAA AAAGTATTGT CGCAAATTCA AATAAAATTT ATTTTCCGCG
2951   CATTGCCAAA ACACAGAAGA TTTGGACTGC GTATCTCGAG GCTATAATGA
3001   AGGTGAGGCA GATGCAGATT CTGAGGCAAC AGATTGCCAA TGAATTAAAT
3051   TATTCTTGTC GGTTTGATTG TAAACATCTG GCAGCTGCTC TGGAGAATCT
3101   CAATAAGGCT CTCCTAGCAG ACATTGAAGC CCACTATCAG GACCCTTCAC
3151   TTCCTTACCC CAAAGAAGAT AACACACTTT TATATGAAAT CACAGCCTAT
3201   CTGGAGGCAG CTGGCATTCA CAACCCACTG AATAAGATAT ACATAACAAC
3251   AAAGCGCTTA CCCTATTTTC CAATTGTAAA CTTTCTATTT TTGATCGCTC
3301   AGTTGCCAAA ACTTCAATAC AACAAAAATC TGGGAATGGT CTGCCGAAAA
3351   CCGACCGACC CGGTTGATTG GCCACCACTT GTCCTGGGAC TGCTACTCTT
3401   GCTGAAGCAG TTCCATTCCC GGTACACCGA GCAGCTCCTG GCGCTGATTG
3451   GCCAGTTTAT CTGCTCCACG GTGGAGCAGT GTACAAGCCA GAAGATACCT
3501   GAAATTCCCTG CAGATGTTGT GGGTGCCCTT CTGTTCTGG AGGATTATGT
3551   TCGGTACACA AAGCTACCCA GGAGGGTTGC TGAAGCACAT GTGCCTAATT
3601   TCATTTTTGA TGAGTTCAGA ACAGTGCTGT AACTGTTTTT CCTACTTCTT
3651   CAATGGAAGG ATTGTCCTTA GATCTTCCCA CCATCACAAA TGAATTTGAA
3701   GATGAAAAGA AACTCAGTTG CTCATACAAC TGCATTTTTT CTGTCTATTA
3751   TGGGAAACAT CAGACGTTAT GAGTAAGATA TATCTCATGG CATTAGTTAA
3801   TATAACTGAT ATTGTTTAAA TCATGGTATT ACATGCAATT TATATCAGAT
3851   AAAAGCAGAA CACATTTTTG TACTGCCTCT CTTAAATGCT GAATGTAAC
3901   GTTATGTATA AATCCATTTA GTTTTATGTT CTAAAGAACT ATTTGTGCAA
3951   CTCCAGATTT TCAGTAAAAT AGTATTACTA GT

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**Figure 12(A)**

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APWRGPADRF FNGGANLSAH LVSSNNIOTP ALRPVNHPQC PGTE•SVRLT
MLDFLAENNL CGQAILRIVS CGNAIIAELL RLSEFIPAVF RLKDRADQOK
YGDIIFFDSY FKGPELWESK LDAKPELQDL DEEFRENNIE IVTRFYLAQ
SVHKYIVDLN RYLDDLNEGV YIQQTLETVL LNEDGKQLLC EALYLYGVML
LVIDQKIEGE VRERMLVSY RYSAARSSAD SNMDDICKLL RSTGYSSQPG
AKRPSNYPES YFQRPINES FISMVIGRLR SDDIYNQVSA YPLPEHRSTA
LANQAAMLYV ILYFEPSILH THQAKMREIV DKYFPDNWVI SIYMGITVNL
VDAWEPYKAA KTALNNTLDL SNVREQASRY ATVSEVHAQ VQQFLKEGYL
REEMVLNIP KLLNCLRDCN VAIRWMLHT ADSACDPNNK RLKQIKDQIL
TDSRYNPRIL FQLLLDTAQF EFILKEMFKQ MLSEKQTKWE HYKKEGSERM
TELADVFSGV KPLTRVEKNE NLQAWFREIS KQILSLNYDD STAAGRKTVO
LIQALEEVQE FHQLESNLQV CQFLADTRKF LHQMIRTINI KEEVLITMQI
VGDLFAWQL IDSFTSIMQE SIRVNPSMVT KLRATFLKLA SALDLPLLR
NQANRPDLLS VSQYYSSELV SYVRKVLQII PESMFTSLK IIKLQTHDII
EVPTRLKDKK LRDYAQLGPR YEVAKLTHAI SIFTEGILMM KTLVGIKIV
DPKQLLEDGI RKELVKRVAF ALHRGLIFNP RAKPSELMK LKELGATMDG
FHRSEFYIQD YVNIYGLKIW QEEVSRIIN NVEQECNNFL RTKIQDWQSM
YQSTHIPIPK FTPVDESVTF IGRLCREILR ITDPKMTCHI DQNTWYDMK
THQEVTSRL FSEIQTTLGT FGLNGLDRL CFMIVKELQN FLSMFQKIIL
RDRTVQDTLK TLMNAVSPK SIVANSNKIY FSAIAKTQKI WTAYLEAIMK
VGQMQLRQQ IANELNYSR FDSKHLAAL ENLNKALLAD IEAHYQDPSL
PYPKEDNTLL YEITAYLEAA GIHNPLNKIY ITTKRLPYFP IVNFLFLIAQ
LPKLQYNKNL GMVCRKPTDP VDWPLVLGL LTLLKQFHSR YTEQLLALIG
QFICSTVEQC TSQKIPEIPA DVVGALLFLE DYVRYTKLPR RVAEAHVPNF
IFDEFRTVL• LFFLLQWKO CP•IFPPSQM NLKMKRNSVA HTTAFFLSIM
GNIRRYE•DI SHGIS•YN•Y CLNHGITCNL YQIKAEHIFV LPLLNACNC
YV•IHLVLCs KELFVQLQIF SKIVLL

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**Figure 12(B)**

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MLDFLAENNL CGQAILRIVS CGNAIIAELL RLSEFIPAVF RLKDRADQQK
YGDIIIFDFS FKGPELWESK LDAKPELQDL DEEFRENNIE IVTRFYLAHQ
SVHKYIVDLN RYLDLNEG VYIQQTLETVL LNEGKQLLC EALYLYGVML
LVIDQKIEGE VRERMLVSY RYSAARSSAD SNMDDICKLL RSTGYSSQPG
AKRPSNYPE S YFQRPINES FISMVIGRLR SDDIYNQVSA YPLPEHRSTA
LANQAAMLYV ILYFEPSILH THQAKMREIV DKYFPDNIWI STYMGITVNL
VDAWEPYKAA KTALNNTLDL SNVREQASRY ATVSEVHAQ VQOFLKEGYL
REEMVLINIP KLINCLRDCN VAIRWMLHT ADSACDPNNK RLKQIKDQIL
TDSRYNPRIL FQLLLDTAQF EFILKEMFKQ MLSEKQTKWE HYKKEGSERM
TELADVFSGV KPLTRVEKNE NLQAWFREIS KQILSLNYDD STAAGRKTQV
LIQALEEVQE FHQLESNLQV CQFLADTRKF LHQMIRTINI KEEVLITMQI
VGDLFAWQL IDSFTSIMQE SIRVNPSMVT KLRATFLKLA SALDPLLLRI
NQANRPDLLS VSQYYSGLV SYVRKVLQII PESMFTSLK IKLQTHDII
EVPTRLKDKK LRDYALGPR YEVAKLTHAI SIFTEGILMM KTTLVGIIKV
DPKQLLEDGI RKELVKRVAF ALHRGLIFNP RAKPSELMK LKELGATMDG
FHRSEFYIQD YVNIYGLKIW QEEVSRIIN NVEQECNNFL RTKIQDWQSM
YQSTHIPIPK FTFVDESFTF IGRLCREILR ITDPKMTCHI DQNTWYDMK
THQEVTSRL FSEIQTTLGT FGLNGLDRLL CFMTVKELQN FLSMFQKII
RDRTVQDTLK TLMNAVSPK SIVANSNKIY FSALAKTQKI WTAYLEADMK
VGQMQLRQQ IANELNYSR FDSKHLAAL ENLNKALLAD IEAHYQDPSL
PYPKEDNTLL YEITAYLEAA GIHNPLNKIY ITTKRLPYFP IVNFLFLIAQ
LPKLQYNKNL GMVCRKPTDP VDWPPVLGL LTLLKQFHSR YTEQLLALIG
QFICSTVEQC TSQKIPEIPA DVVGALLFLE DYVRYTKLPR RVAEAVPNF
IFDEFRTVL

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**Figure 13(A)**

AGG GGC GGA AGT CGG GGT CTG ACC CGC TCC AGG TCC GGG ACT GCG GAT  
 AGA AGA GGA CCG CCG CCT TGA GGG AGG GGT GGA AAC TGG GTG CCG GCT  
 CCG CGC GCG ACC TCC GGC CCT GCG CGT GCG CCG TGG CGC GGC CCG GCT  
 GAC AGG TTC TTT AAT GGA GGA GCC AAT CTC TCT GCA CAC CTG GTT TCA  
 TCT AAT AAT ATA CAG ACA CCA GCT CTG AGG CCA GTT AAT CAT CCC CAG  
 TGT CCA GGC ACA GAG TAG TCG GTC CGC CTC ACA ATG TTG GAC TTT CTA  
 GCC GAG AAC AAC CTC TGT GGC CAA GCA ATC CTA AGG ATT GTT TCC TGT  
 GGT AAT GCC ATC ATT GCT GAA CTT TTG AGA CTC TCT GAG TTT ATT CCT  
 GCT GTG TTC AGG TTA AAA GAC AGA GCT GAT CAA CAG AAA TAT GGA GAT  
 ATC ATA TTT GAT TTC AGC TAT TTT AAG GGT CCA GAA TTA TGG GAA AGC  
 AAA CTG GAT GCT AAG CCA GAG CTA CAG GAT TTA GAT GAA GAA TTT CGT  
 GAA AAC AAC ATA GAA ATT GTG ACC AGA TTT TAT TTA GCA TTT CAA AGT  
 GTA CAT AAA TAT ATT GTA GAC TTA AAC AGA TAT CTA GAT GAT CTC AAT  
 GAA GGG GTT TAT ATT CAG CAA ACC TTA GAA ACT GTG CTT CTC AAT GAA  
 GAT GGA AAA CAA CTT CTA TGT GAA GCA CTG TAC TTA TAT GGA GTT ATG  
 CTA CTG GTC ATT GAC CAA AAG ATT GAA GGA GAA GTC AGA GAG AGG ATG  
 CTG GTT TCT TAC TAC CGA TAC AGT GCT GCT CGA TCT TCT GCT GAT TCA  
 AAT ATG GAC GAT ATT TGT AAG CTG CTT CGA AGT ACA GGT TAT TCT AGC  
 CAA CCA GGT GCC AAA AGA CCA TCC AAC TAT CCC GAG AGC TAT TTC CAG  
 AGA GTG CCT ATC AAC GAA TCC TTC ATC AGT ATG GTC ATT GGT CGA CTG  
 AGA TCT GAT GAT ATT TAC AAC CAG GTC TCA GCG TAT CCT TTG CCG GAG  
 CAT CGC AGC ACA GCC CTG GCA AAC CAA GCT GCC ATG CTG TAC GTG ATT  
 CTC TAC TTT GAG CCT TCC ATC CTT CAC ACC CAT CAA GCA AAA ATG AGA  
 GAG ATA GTG GAT AAA TAC TTT CCA GAT AAT TGG GTA ATT AGT ATT TAC  
 ATG GGG ATC ACA GTT AAT CTA GTA GAT GCT TGG GAA CCT TAC AAA GCT  
 GCA AAA ACT GCT TTA AAT AAT ACC CTG GAC CTT TCA AAT GTC AGA GAA  
 CAG GCA AGC AGA TAT GCT ACT GTC AGT GAA AGA GTG CAT GCT CAA GTG  
 CAG CAA TTT CTA AAA GAA GGT TAT TTA AGG GAG GAG ATG GTT CTG GAC  
 AAT ATC CCA AAG CTT CTG AAC TGC CTG AGA GAC TGC AAT GTT GCC ATC  
 CGA TGG CTG ATG CTT CAT ACA GCA GAC TCA GCC TGT GAC CCA AAC AAC  
 AAA CGC CTT CGT CAA ATC AAG GAC CAG ATT CTA ACA GAC TCT CGG TAC  
 AAT CCC AGG ATC CTC TTC CAG CTG CTT TTA GAT ACT GCA CAA TTT GAG  
 TTT ATA CTC AAA GAG ATG TTC AAG CAA ATG CTT TCA GAA AAG CAA ACC  
 AAA TGG GAG CAT TAC AAG AAA GAG GGT TCG GAG CGG ATG ACT GAG CTT  
 GCT GAT GTC TTT TCA GGA GTG AAA CCC CTA ACC AGA GTG GAG AAA AAT  
 GAA AAC CTT CAA GCT TGG TTC AGA GAG ATC TCA AAA CAA ATA TTG TCT  
 TTA AAT TAT GAT GAT TCT ACT GCT GCG GGC AGA AAA ACT GTA CAA CTG  
 ATA CAA GCT TTG GAA GAG GTT CAA GAA TTC CAC CAG TTG GAA TCC AAT  
 CTG CAA GTA TGT CAG TTT CTT GCC GAT ACT CGA AAG TTT CTT CAT CAA  
 ATG ATC AGA ACC ATT AAC ATT AAA GAG GAG GTT CTG ATC ACA ATG CAG  
 ATC GTT GGG GAC CTT TCT TTC GCT TGG CAG TTG ATT GAC AGT TTC ACA  
 TCC ATC ATG CAA GAA AGC ATA AGG GTA AAT CCA TCC ATG GTT ACT AAA  
 CTC AGA GCT ACC TTC CTA AAG CTT GCC TCT GCC CTC GAT CTG CCC CTT  
 CTT CGT ATT AAT CAG GCA AAT CGC CCC GAC CTG CTC AGC GTG TCA CAG  
 TAC TAT TCT GGA GAG TTG GTA TCC TAT GTG AGA AAA GTT TTG CAG ATC  
 ATC CCA GAA AGC ATG TTT ACA TCT CTT CTA AAG ATC ATA AAG CTT CAG  
 ACC CAC GAC ATT ATT GAA GTG CCT ACC CGC CTG GAC AAA GAC AAG CTG  
 AGG GAC TAT GCT CAG CTA GGC CCA CGA TAC GAG GTT GCC AAG CTT ACT  
 CAT GCT ATT TCC ATT TTT ACT GAA GGC ATC TTA ATG ATG AAA ACG ACT



Figure 13(B)

TTG GTT GGC ATC ATC AAG GTG GAT CCA AAG CAG TTG CTG GAA GAT GGA  
ATA AGG AAA GAG CTT GTG AAG CGC GTT GCC TTT GCC CTG CAT AGG GGA  
CTG ATA TTC AAC CCT CGA GCC AAG CCA AGT GAA TTG ATG CCC AAG CTG  
AAA GAG TTG GGA GCG ACC ATG GAT GGA TTC CAT CGT TCT TTT GAA TAC  
ATA CAG GAC TAT GTC AAC ATT TAT GGT CTG AAG ATT TGG CAG GAA GAA  
GTA TCT CGT ATC ATA AAT TAC AAC GTG GAG CAA GAG TGT AAT AAC TTT  
CTA AGA ACG AAG ATT CAA GAT TGG CAA AGC ATG TAC CAG TCC ACT CAT  
ATT CCA ATA CCC AAG TTT ACC CCT GTG GAT GAG TCT GTA ACG TTT ATT  
GGT CGA CTC TGC AGA GAA ATC CTG CGG ATC ACA GAC CCA AAA ATG ACA  
TGT CAC ATA GAC CAG CTG AAC ACT TGG TAT GAT ATG AAA ACT CAT CAG  
GAA GTG ACC AGC AGC CGC CTC TTC TCA GAA ATC CAG ACC ACC TTG GGA  
ACC TTT GGT CTA AAT GGC TTA GAC AGG CTT CTG TGC TTT ATG ATT GTA  
AAA GAG TTA CAG AAT TTC CTC AGT ATG TTT CAG AAA ATT ATC CTG AGA  
GAC AGA ACT GTT CAG GAC ACT TTA AAA ACC CTC ATG AAT GCT GTC AGT  
CCC CTA AAA AGT ATT GTC GCA AAT TCA AAT AAA ATT TAT TTT TCC GCC  
ATT GCC AAA ACA CAG AAG ATT TGG ACT GCG TAT CTC GAG GCT ATA ATG  
AAG GTT GGG CAG ATG CAG ATT CTG AGG CAA CAG ATT GCC AAT GAA TTA  
AAT TAT TCT TGT CGG TTT GAT TCT AAA CAT CTG GCA GCT GCT CTG GAG  
AAT CTC AAT AAG GCT CTC CTA GCA GAC ATT GAA GCC CAC TAT CAG GAC  
CCT TCA CTT CCT TAC CCC AAA GAT AAC ACA CTT TTA TAT GAA ATC  
ACA GCC TAT CTG GAG GCA GCT GGC ATT CAC AAC CCA CTG AAT AAG ATA  
TAC ATA ACA ACA AAG CGC TTA CCC TAT TTT CCA ATT GTA AAC TTT CTA  
TTT TTG ATC GCT CAG TTG CCA AAA CTT CAA TAC AAC AAA AAT CTG GGA  
ATG GTC TGC CGA AAA CCG ACC GAC CCG GTT GAT TGG CCA CCA CTT GTC  
CTG GGA CTG CTC ACT CTG CTG AAG CAG TTC CAT TCC CGG TAC ACC GAG  
CAG CTC CTG GCG CTG ATT GGC CAG TTT ATC TGC TCC ACG GTG GAG CAG  
TGT ACA AGC CAG AAG ATA CCT GAA ATT CCT GCA GAT GTT GTG GGT GCC  
CTT CTG TTC CTG GAG GAT TAT GTT CGG TAC ACA AAG CTA CCC AGG AGG  
GTT GCT GAA GCA CAT GTG CCT AAT TTC ATT TTT GAT GAG TTC AGA ACA  
GTG CTG TAA CTG TTT TTC CTA CTT CTT CAA TGG AAG GAT TGT CCT TAG  
ATC TTC CCA CCA TCA CAA ATG AAT TTG AAG ATG AAA AGA AAC TCA GTT  
GCT CAT ACA ACT GCA TTT TTT CTG TCT ATT ATG GGA AAC ATC AGA CGT  
TAT GAG TAA GAT ATA TCT CAT GGC ATT AGT TAA TAT AAC TGA TAT TGT  
TTA AAT CAT GGT ATT ACA TGC AAT TTA TAT CAG ATA AAA GCA GAA CAC  
ATT TTT GTA CTG CCT CTC TTA AAT GCT GAA TGT AAC TGT TAT GTA TAA  
ATC CAT TTA GTT TTA TGT TCT AAA GAA CTA TTT GTG CAA CTC CAG ATT  
TTC AGT AAA ATA GTA TTA CTA GT

**Figure 14(A)**

Arg Gly Gly Ser Arg Gly Leu Thr Arg Ser Arg Ser Gly Thr Ala Asp  
 Arg Arg Gly Pro Pro Pro \* Gly Arg Gly Gly Asn Trp Val Pro Ala  
 Pro Arg Ala Thr Ser Gly Pro Ala Arg Ala Pro Trp Arg Gly Pro Ala  
 Asp Arg Phe Phe Asn Gly Gly Ala Asn Leu Ser Ala His Leu Val Ser  
 Ser Asn Asn Ile Gln Thr Pro Ala Leu Arg Pro Val Asn His Pro Gln  
 Cys Pro Gly Thr Glu \* Ser Val Arg Leu Thr Met Leu Asp Phe Leu  
 Ala Glu Asn Asn Leu Cys Gly Gln Ala Ile Leu Arg Ile Val Ser Cys  
 Gly Asn Ala Ile Ile Ala Glu Leu Leu Arg Leu Ser Glu Phe Ile Pro  
 Ala Val Phe Arg Leu Lys Asp Arg Ala Asp Gln Gln Lys Tyr Gly Asp  
 Ile Ile Phe Asp Phe Ser Tyr Phe Lys Gly Pro Glu Leu Trp Glu Ser  
 Lys Leu Asp Ala Lys Pro Glu Leu Gln Asp Leu Asp Glu Glu Phe Arg  
 Glu Asn Asn Ile Glu Ile Val Thr Arg Phe Tyr Leu Ala Phe Gln Ser  
 Val His Lys Tyr Ile Val Asp Leu Asn Arg Tyr Leu Asp Asp Leu Asn  
 Glu Gly Val Tyr Ile Gln Gln Thr Leu Glu Thr Val Leu Leu Asn Glu  
 Asp Gly Lys Gln Leu Leu Cys Glu Ala Leu Tyr Leu Tyr Gly Val Met  
 Leu Leu Val Ile Asp Gln Lys Ile Glu Gly Glu Val Arg Glu Arg Met  
 Leu Val Ser Tyr Tyr Arg Tyr Ser Ala Ala Arg Ser Ser Ala Asp Ser  
 Asn Met Asp Asp Ile Cys Lys Leu Arg Ser Thr Gly Tyr Ser Ser  
 Gln Pro Gly Ala Lys Arg Pro Ser Asn Tyr Pro Glu Ser Tyr Phe Gln  
 Arg Val Pro Ile Asn Glu Ser Phe Ile Ser Met Val Ile Gly Arg Leu  
 Arg Ser Asp Asp Ile Tyr Asn Gln Val Ser Ala Tyr Pro Leu Pro Glu  
 His Arg Ser Thr Ala Leu Ala Asn Gln Ala Ala Met Leu Tyr Val Ile  
 Leu Tyr Phe Glu Pro Ser Ile Leu His Thr His Gln Ala Lys Met Arg  
 Glu Ile Val Asp Lys Tyr Phe Pro Asp Asn Trp Val Ile Ser Ile Tyr  
 Met Gly Ile Thr Val Asn Leu Val Asp Ala Trp Glu Pro Tyr Lys Ala  
 Ala Lys Thr Ala Leu Asn Asn Thr Leu Asp Leu Ser Asn Val Arg Glu  
 Gln Ala Ser Arg Tyr Ala Thr Val Ser Glu Arg Val His Ala Gln Val  
 Gln Gln Phe Leu Lys Glu Gly Tyr Leu Arg Glu Glu Met Val Leu Asp  
 Asn Ile Pro Lys Leu Leu Asn Cys Leu Arg Asp Cys Asn Val Ala Ile  
 Arg Trp Leu Met Leu His Thr Ala Asp Ser Ala Cys Asp Pro Asn Asn  
 Lys Arg Leu Arg Gln Ile Lys Asp Gln Ile Leu Thr Asp Ser Arg Tyr  
 Asn Pro Arg Ile Leu Phe Gln Leu Leu Leu Asp Thr Ala Gln Phe Glu  
 Phe Ile Leu Lys Glu Met Phe Lys Gln Met Leu Ser Glu Lys Gln Thr  
 Lys Trp Glu His Tyr Lys Lys Glu Gly Ser Glu Arg Met Thr Glu Leu  
 Ala Asp Val Phe Ser Gly Val Lys Pro Leu Thr Arg Val Glu Lys Asn  
 Glu Asn Leu Gln Ala Trp Phe Arg Glu Ile Ser Lys Gln Ile Leu Ser  
 Leu Asn Tyr Asp Asp Ser Thr Ala Ala Gly Arg Lys Thr Val Gln Leu  
 Ile Gln Ala Leu Glu Glu Val Gln Glu Phe His Gln Leu Glu Ser Asn  
 Leu Gln Val Cys Gln Phe Leu Ala Asp Thr Arg Lys Phe Leu His Gln  
 Met Ile Arg Thr Ile Asn Ile Lys Glu Glu Val Leu Ile Thr Met Gln  
 Ile Val Gly Asp Leu Ser Phe Ala Trp Gln Leu Ile Asp Ser Phe Thr  
 Ser Ile Met Gln Glu Ser Ile Arg Val Asn Pro Ser Met Val Thr Lys  
 Leu Arg Ala Thr Phe Leu Lys Leu Ala Ser Ala Leu Asp Leu Pro Leu  
 Leu Arg Ile Asn Gln Ala Asn Arg Pro Asp Leu Leu Ser Val Ser Gln  
 Tyr Tyr Ser Gly Glu Leu Val Ser Tyr Val Arg Lys Val Leu Gln Ile  
 Ile Pro Glu Ser Met Phe Thr Ser Leu Leu Lys Ile Ile Lys Leu Gln  
 Thr His Asp Ile Ile Glu Val Pro Thr Arg Leu Asp Lys Asp Lys Leu  
 Arg Asp Tyr Ala Gln Leu Gly Pro Arg Tyr Glu Val Ala Lys Leu Thr  
 His Ala Ile Ser Ile Phe Thr Glu Gly Ile Leu Met Met Lys Thr Thr  
 Leu Val Gly Ile Ile Lys Val Asp Pro Lys Gln Leu Leu Glu Asp Gly  
 Ile Arg Lys Glu Leu Val Lys Arg Val Ala Phe Ala Leu His Arg Gly

**Figure 14(B)**

Leu Ile Phe Asn Pro Arg Ala Lys Pro Ser Glu Leu Met Pro Lys Leu  
 Lys Glu Leu Gly Ala Thr Met Asp Gly Phe His Arg Ser Phe Glu Tyr  
 Ile Gln Asp Tyr Val Asn Ile Tyr Gly Leu Lys Ile Trp Gln Glu Glu  
 Val Ser Arg Ile Ile Asn Tyr Asn Val Glu Gln Glu Cys Asn Asn Phe  
 Leu Arg Thr Lys Ile Gln Asp Trp Gln Ser Met Tyr Gln Ser Thr His  
 Ile Pro Ile Pro Lys Phe Thr Pro Val Asp Glu Ser Val Thr Phe Ile  
 Gly Arg Leu Cys Arg Glu Ile Leu Arg Ile Thr Asp Pro Lys Met Thr  
 Cys His Ile Asp Gln Leu Asn Thr Trp Tyr Asp Met Lys Thr His Gln  
 Glu Val Thr Ser Ser Arg Leu Phe Ser Glu Ile Gln Thr Thr Leu Gly  
 Thr Phe Gly Leu Asn Gly Leu Asp Arg Leu Leu Cys Phe Met Ile Val  
 Lys Glu Leu Gln Asn Phe Leu Ser Met Phe Gln Lys Ile Ile Leu Arg  
 Asp Arg Thr Val Gln Asp Thr Leu Lys Thr Leu Met Asn Ala Val Ser  
 Pro Leu Lys Ser Ile Val Ala Asn Ser Asn Lys Ile Tyr Phe Ser Ala  
 Ile Ala Lys Thr Gln Lys Ile Trp Thr Ala Tyr Leu Glu Ala Ile Met  
 Lys Val Gly Gln Met Gln Ile Leu Arg Gln Gln Ile Ala Asn Glu Leu  
 Asn Tyr Ser Cys Arg Phe Asp Ser Lys His Leu Ala Ala Ala Leu Glu  
 Asn Leu Asn Lys Ala Leu Leu Ala Asp Ile Glu Ala His Tyr Gln Asp  
 Pro Ser Leu Pro Tyr Pro Lys Glu Asp Asn Thr Leu Leu Tyr Glu Ile  
 Thr Ala Tyr Leu Glu Ala Ala Gly Ile His Asn Pro Leu Asn Lys Ile  
 Tyr Ile Thr Thr Lys Arg Leu Pro Tyr Phe Pro Ile Val Asn Phe Leu  
 Phe Leu Ile Ala Gln Leu Pro Lys Leu Gln Tyr Asn Lys Asn Leu Gly  
 Met Val Cys Arg Lys Pro Thr Asp Pro Val Asp Trp Pro Pro Leu Val  
 Leu Gly Leu Leu Thr Leu Leu Lys Gln Phe His Ser Arg Tyr Thr Glu  
 Gln Leu Leu Ala Leu Ile Gly Gln Phe Ile Cys Ser Thr Val Glu Gln  
 Cys Thr Ser Gln Lys Ile Pro Glu Ile Pro Ala Asp Val Val Gly Ala  
 Leu Leu Phe Leu Glu Asp Tyr Val Arg Tyr Thr Lys Leu Pro Arg Arg  
 Val Ala Glu Ala His Val Pro Asn Phe Ile Phe Asp Glu Phe Arg Thr  
 Val Leu \* Leu Phe Phe Leu Leu Leu Gln Trp Lys Asp Cys Pro \*  
 Ile Phe Pro Pro Ser Gln Met Asn Leu Lys Met Lys Arg Asn Ser Val  
 Ala His Thr Thr Ala Phe Phe Leu Ser Ile Met Gly Asn Ile Arg Arg  
 Tyr Glu \* Asp Ile Ser His Gly Ile Ser \* Tyr Asn \* Tyr Cys  
 Leu Asn His Gly Ile Thr Cys Asn Leu Tyr Gln Ile Lys Ala Glu His  
 Ile Phe Val Leu Pro Leu Leu Asn Ala Glu Cys Asn Cys Tyr Val \*  
 Ile His Leu Val Leu Cys Ser Lys Glu Leu Phe Val Gln Leu Gln Ile  
 Phe Ser Lys Ile Val Leu Leu

**Figure 15**

+ strand (sense)		sequence (5'-->3')
1. pch13-sp6-1f	1st base 370	TTT ACT TCT AAC GCT TAT TC
2. pch13-sp6-2f	726	TGA AGG AGT CCT TTG AGA CG
3. T7.1	1140	TCA CAA TGG GCT ACT GG
4. T7.2	1361	TTC AAC GAG GGA GAT GG
5. T7.3	1602	TTA GCA CCA CTG AGA GA
6. T7.4	2041	GTT CTT TTA GGC ATT TA
7. ch13-2480	2486	GCT GCG TCT GTT CGT CAG C
- strand (antisense)		
8. SP6.1	2746	CCT CTG CTT CAC AAC AT
9. SP6.2	2490	GCA GtA GGG CGG ACA CC
10. SP6.3	2213	(C) AGG GTC TTC TTC ATT GT
11. SP6.4	1812	GGA TTG TCT TTG TCT CT
12. pch13-t7-1f	1165	AGT GCA CTT CCA TGG GCG TG
13. pch13-t7-1fa	712	CCT TCA TCA GGT TGA CGA AC
14. pch13-t7-2fa	286	GCG GCA ATC AGA AAC GGA AG
15. CH13-AS-1	536	TGA ACA CGT GGT ACA T

Figure 16(A)

1	CTTCCCTGAG	CCCTTTCTGC	CTGTGTAGGA	AGCAGAAGGC	GGAATGTCCG
51	CTCTGCCCTT	CTCCGTAAGA	TGGTGCATTA	AAACGTTCCCT	TATAAACTGG
101	AAATGAAGGC	TGCGGAAGAT	GGCTAAAATC	AGCAATCCTT	GGAATAACGC
151	AGAAGCATCC	CTGCTTCCCT	GGGCCCGCCC	GTGGGCCTGC	TTGTGCTGTT
201	CAGTAGGTGG	TTTTTAGAAA	GGGCTTCCTT	CAGCGTCATT	AGCAACAGGA
251	GTCGTCTGCC	GTTTGCATGA	GGAAATGTTT	TTAACCTTCC	GTTTCTGATT
301	GCCTCTAGAC	TGCATCTGTC	ATAGACAAAT	GCCCCATCT	TTTACAGAGA
351	ACCAGTCTCT	TCTTTAAACT	TTACTTCTAA	CGCTTATTCT	TTTTACCTTA
401	TATAGGAAAC	CACTGATTGC	TTGTGTGGAG	AAACAGCTAT	TAGGAGAACA
451	TTTAACAGCA	ATTCTGCAGA	AAGGGCTCGA	CCACTTACTG	GATGAGAACA
501	GAGTGCCGGA	CCTCGCACAG	ATGTACCAGC	TGTTTCAGCCG	GGTGAGGGGC
551	GGGCAGCAGG	CGCTGCTGCA	GCACCTGGAGC	GAGTACATCA	AGACTTTTGG
601	AACAGCGATC	GTAATCAATC	CTGAGAAAGA	CAAAGACATG	GTCCAAGACC
651	TGTTGGACTT	CAAGGACAAG	GTGGACCACG	TGATCGAGGT	CTGCTTCCAG
701	AAGAAAGAGC	GGTTCGTCAA	CCTGATGAAG	GAGTCCTTTG	AGACGTTTCT
751	CAACAAGAGA	CCCAACAAGC	CTGCAGAACT	GATCGCAAAG	CATGTGGATT
801	CAAAGTTAAG	AGCAGGCAAC	AAAGAAGCCA	CAGACGAGGA	GCTGGAGCCG
851	ACGTGCGACA	AGATCATGAT	CCTGTTTCAGG	TTTATCCACG	GTAAGATGTT
901	CTTTGAAGCA	TTTTTATAAA	AAGATTGTCG	AAAAAGACTC	CTTGTGGGGA
951	AAAGTGCCCT	AGTCGATGCT	GAAAAGTCTA	TGTTGTCAAA	GCTCAAGCAT
1001	GAGTGCGGTG	CAGCCTTCAC	CAGCAAGCTG	GAAGGCATGT	TCAAGGACAT
1051	GGAGCTTTTC	AAGGACATCA	TGGTTCATTT	CAAGCAGCAT	ATGCAGAAATC
1101	AGAGTGACTC	AGGCCCTATA	GACCTCACAG	TGAACATACT	CACAATGGGC
1151	TACTGGCCAA	CATACACGCC	CATGGAAGTG	CACTTAACCC	CAGAAATGAT
1201	TAAACTTCAG	GAAGTATTTA	AGGCATTTTA	TCTTGGAAAG	CACAGTGGTC
1251	GAAAACTTCA	GTGGCAAAC	ACTTTGGGAC	ATGCTGTTTT	AAAAGCGGAG
1301	TTTAAAGAAG	GGAAGAAGGA	ATTCCAGGTG	TCCCTCTTCC	AGACACTGGT
1351	GCTCCTCATG	TTCAACGAGG	GAGATGGCTT	CAGCTTTGAG	GAGATAAAAA
1401	TGGCCACGGG	GATAGAGGAT	AGTGAATTGC	GCAGAACGCT	GCAGTCCCTG
1451	GCCTGTGGCA	AAGCACGTGT	GCTGATTAAA	AGTCCCAAAG	GAAAGGAAGT
1501	GGAAGATGGA	GACAAGTTCA	TTTTTAATGG	AGAGTTCAAG	CACAAGTTGT
1551	TTAGAATAAA	GATCAATCAA	ATTTCAGATGA	AGGAACTGT	TGAGGAACAG
1601	GTTAGCACCA	CTGAGAGAGT	GTTTCAGGAT	AGACAATATC	AGATTGATGC
1651	TGCTATCGTC	AGAATAATGA	AGATGAGAAA	GACTCTTGGT	CATAATCTTC
1701	TAGTTTCTGA	ATTATATAAT	CAGCTGAAAT	TTCCAGTAAA	GCCTGGAGAT
1751	TTGAAAAAGA	GAATTGAATC	TCTGATAGAC	AGAGACTATA	TGGAGAGAGA
1801	CAAAGACAAT	CCGAATCAGT	ACCACTACGT	GGCCTGACGC	ATCTGCAGAC
1851	GGTTCCCTTT	CATGAAACAC	TAGAATGTAC	CCTCAGAGCA	GGAAGCACAC
1901	CTGTGCCATT	TCTGGGACTC	TGATTGATCC	AGCTGTGGAC	ATTGGAAGGC
1951	GAAGGAAGGG	AGGTGGCTCC	TGGGTATCT	TTTCAAGGC	TCAAGACTTC
2001	AACCTGCAGA	TGTATCTTTT	TCCCTCCAGT	TTTTCTCTTA	GTTCTTTTAG
2051	GCATTTAAAT	TGTTTCTGTT	ACTCTGTGCA	AAATAACTTT	GAGATTGGAC
2101	AAGAAGATGT	TACTAAAGAG	AAGTTCCCTT	AAAAGGTCTT	GTTCTTGTGT
2151	CAAAAAGCTG	CAAGTTTGGT	TTGTTCTCGT	GTGTGATCAT	GAGTGCACAA
2201	TGAAGAAGAC	CCTAGATGCT	GCATTTTFTA	GCTCTGAAGA	TTCTTTAGGT
2251	ATCCCTGAAG	ACAGCTCGCT	CAGATGATCA	GCATTTAGAG	TGAAAACAAG
2301	GGCCCTTCAT	GGGTGAACAT	TAGAAAGAGC	CAGGGTTCAA	AGCTGGCGAA
2351	TGGATGACGC	ACCCTAGCCA	CTGGCCCTC	CCTGTTTCAT	GTATTTCCAA
2401	AAGTTGTAAA	CTTGGGTGGC	TGATTTTTTCG	TAAGTCAGGT	TTCTAAGTGA
2451	GCTCCCTGAG	GTGCCAAGGC	CATGGTGTCC	GCCCTGCTGC	GTCTGTTCGT
2501	CAGCTGAGTT	CCTTGTGAAT	CTCTGTTTTA	GGGGTTGGGG	CTAGTGTGTT

**Figure 16(B)**

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2551   TGTGTTTCCA TTCTAAGATT GAGTCTGGCA GTCCCTGTTT TTTTGCATTG
2601   GGGTAACTGC TCTTTGATTT TTTTAAATG CAGTATTTGT GTGATTGCAA
2651   TAATAAAGTT TGGTTTGGTT TTTACAGTCA TGCGCAGGGA CGATCCTTGT
2701   TCTCTGCTGT AAACGTGAAA AAGTTTATGG AGACCTAAAG TCTTGATGTT
2751   GTGAAGCAGA GGTATTTTGG TGGAAAGATT AAAAGGATTT TGTGTTGTTACC
2801   TGGTTTTGTG TTGTGTATAT ATACATGAGG TTGAACAGTG AAAGGAAAGT
2851   TCAGTAGTGA TGTTAGAAGG GTAACATGA CAAAGATACT TTTGAGATAA
2901   CATTTAAAAG TACTTTATAT TTTACATAAT AGCATGTTTC ATTTTGATTA
2951   AAAGCTACCA AAGGAATTTT GATCATGGCA TAAGTGTTTA AAGCAATATT
3001   TTCTGGAATA TACCAAGTTT ATATAATTTG ATTTTGTGCT AAATTATTAA
3051   GAGTCTCTTT TTGAAACATG CGGGTTTGAA ATATGACACC TTGTGGGTTT
3101   CCATATTAAA ATCCTCACTC TTTAATTGTC ATTTTATCT TTGAAAATTT
3151   TCATTTATGA GTTCCATGAT ATGTGGTCTA AGAAAGACCA AACAGATTTT
3201   TATTTTTTTT TCTTATAAGT TCGTTGTGTC TAGAGATTGT TAATATTGTA
3251   ATTTAATGTA GACTTACTTT GAATAAAATT AGTTTAATTG GCCTTAAAT
3301   TACATTAATA AAACTTGTG ATATGCAAAT GACACATTC
```

**Figure 17**

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1      FPEPFLPV·E AEGGMSALPF SVRWCIKTFL INWK·RLGKM AKISNPWNNNA
51     EASLLPWARP WACLCSSVGG F·KGLPSASL ATGVVVRLE EMFLTFRF·L
101    PLDCICHRQM PPSFTENQSL L·TLLLTLIL FTLVRKPLIA CVEKQLLGEH
151    LTAILQKGLD HLLDENRVPD LAQMYQLFSR VRGGQOALLQ HWSEYIKTFG
201    TATIVINPEKD KDMVQDLLDF KDKVDHVIEV CFQKNERFVN LMKESFETFI
251    NKRPNKPAEL IAKHVDSKLR AGNKEATDEE LERTLDKIMI LFRFIHGKDV
301    FEAIFYKDLA KRLLVGKSAS VDAEKSMLSK LKHECGAAFT SKLEGMFKDM
351    ELSKDIMVHF KQHMNQSDS GPIDLTVNIL TMGYWPTYTP MEVHLTPEMI
401    KLQEVFKAFY LGKHSGRKLQ WQTTLGHAVL KAEFKEGKKE FQVSLFQTLV
451    LLMFNEGDGF SFEEIKMATG IEDSELRRTL QSLACGKARV LIKSPKGKEV
501    EDGDKFIFNG EFKHKLFRK INQIQMKETV EEQVSTTERV FQDRQYQIDA
551    AIVRIMMRK TLGHNLLVSE LYNQLKFPVK PGDLKKRIES LIDRDYMERD
601    KINPNQYHYV A·RICRRFPF MKH·NVPSEQ EAHLCWFWS D·SSCGHWKA
651    KEGRWLLGHL SQGSRLQPAD VSFSLQFFL· FF·AFKLFL LCAK·L·DWT
701    RRCY·REVPL KGLVLVSKSC KFGLFSCVIM SAQ·RRP·ML HFLALKIP·V
751    SLKTARSDDQ HLE·KQGPFM GEH·KEPGFK AGEWMTHPSH WPLPVSCISK
801    SCKLWWLIFR KSGF·VSSLR CQGHGVRPAA SVRQLSSL·I SVLGVGASVF
851    VFPP·D·VWQ SLFFCIGVTA L·FFLIADFV ·LQ··SLVWF LQSCAGTILV
901    LCCKL·KVYG DLKS·CCEAE VILWKD·KDF VGTWFCVVYI YMRLNSERKV
951    Q··C·KGNVD KDTFEITFKS TLYFT··HVS F·LKATKGIL IMA·VFKAIF
1001   SGIYQVYII· FCAKLLRVSF ·NMRV·NMTP CGFPY·NPHS LIVIFIFENF
1051   HL·VP·YVV· ERPNRFLFFF LISSLCLTEV NIVI·CRLTL NKISLIGLKI
1101   TLIKLCMDQM TH

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201    TATIVINPEKD KDMVQDLLDF MYQLFSR VRGGQOALLQ HWSEYIKTFG
251    NKRPNKPAEL IAKHVDSKLR KDKVDHVIEV CFQKNERFVN LMKESFETFI
301    FEAIFYKDLA KRLLVGKSAS AGNKEATDEE LERTLDKIMI LFRFIHGKDV
351    ELSKDIMVHF KQHMNQSDS VDAEKSMLSK LKHECGAAFT SKLEGMFKDM
401    KLQEVFKAFY LGKHSGRKLQ GPIDLTVNIL TMGYWPTYTP MEVHLTPEMI
451    LLMFNEGDGF SFEEIKMATG WQTTLGHAVL KAEFKEGKKE FQVSLFQTLV
501    EDGDKFIFNG EFKHKLFRK IEDSELRRTL QSLACGKARV LIKSPKGKEV
551    AIVRIMMRK TLGHNLLVSE INQIQMKETV EEQVSTTERV FQDRQYQIDA
601    KINPNQYHYV A PGDLKKRIES LIDRDYMERD

```

**Figure 18**

+ strand (sense)		sequence (5'-->3')	
	1st base		
1. pch14-sp6-1f	686	GGC TTA ACA CTC AAT GTA C	
2. pch14-sp6-2f	1005	CTA TGA AAA GAC AGC TTA AG	
3. pch14-SP6-3f	1315	ATT TAG TTT GAA AAG CAT G	
4. pch14-sp6-4f	1589	CAG ACT TTA AAG TCA CAA G	
5. pch14-sp6-5f	1808	CAA AGA CTT GGT GTA TAG TG	
- strand (antisense)		sequence (5'-->3')	
6. pch14-sp6-6fb	2020	GCA GTT TAA TTT GGT CCT G	
7. pch14-sp6-5fb	1757	CTG TAA TTA TAG TTC TGT C	
8. pch14-sp6-4fb	1607	CTT GTG ACT TTA AAG TCT G	
9. pch14-sp6-3fb	1339	ATA ATC ATG CTT TTC AAA C	
10. pch14-sp6-2rb	1023	TTA AGC TGT CTT TTC ATA G	
11. pch14-sp6-1rb	704	GTA CAT TGA GTG TTA AAC C	
12. CH14a	629	CGG CAG AGC TGA CTA CTG GAA GG	
13. CH14b	644	CAA GCA GGG AAG TAA CGG CAG	
14. CH14c	109	CTT GTT AGC TTG TTT AGA AGG	
		TGG AAG AG	
15. CH14d	90	GGT GGA AGA GAA GGT CTC CTT	
		TCA GGC	



Figure 19

1	GAAGATGATG	ATTACGGGTC	TCGAACAGGA	AGCATCTCCA	GCAGTGTGTC
51	TGTGCCTGCA	AAGCCTGAAA	GGAGACCTTC	TCTTCCACCT	TCTAAACAAG
101	CTAACAAGAA	TCTGATTTTG	AAGGCTATAT	CTGAAGCTCA	AGAATCCGTA
151	ACAAAAACAA	CTAACTACTC	TACAGTTCCA	CAGAAACAGA	CACTTCCAGT
201	TGCTCCCAGA	ACTCGAACTT	CTCAAGAAGA	ATTGCTAGCA	GAAGTGGTCC
251	AGGGACAAAG	TAGGACCCCC	AGAATAAGTC	CCCCATTAA	AGAAGAGGAA
301	ACAAAAGGAG	ATTCTGTAGA	AAAAAATCAA	GCTGAGATGA	GTGAACTGAG
351	TGTGGCACAG	AAACCAGAAA	AACTTTTGGG	GCGCTGCAAG	TACTGGCCTG
401	CTTGTAAGAAA	TGGGGATGAG	TGTGCCTACC	ATCACCCCAT	CTCACCCCTG
451	AAAGCCTTCC	CCAATTGTAA	ATTTGCTGAA	AAATGTTTGT	TTGTTTCAACC
501	AAATGTGAAA	TATGATGCAA	AGTGTACTAA	ACCAGATGTG	CCCTTCACTC
551	ATGTGAGTAG	AAGAATTCCA	GTACTGTCTC	CAAAACCAGT	TGCACCACCA
601	GCACCACCTT	CCAGTAGTCA	GCTCTGCCGT	TACTTCCCTG	CTTGTAAGAA
651	GATGGAATGT	CCCTTCTATC	ATCCAAAACA	TTGTAGGTTT	AACACTCAAT
701	GTACAAGTCC	GGACTGCACA	TTCTACCATC	CCACCATTAA	TGTCACCA
751	CGACATGCCT	TGAAATGGAT	TCGACCTCAA	ACCAGCGAAT	AGCACCCAGT
801	CCTGCCTGGC	AGAAGATCAT	GCAGTTTGGG	AGTTTTCATG	TACTGATGAA
851	AGATACTCTA	CAGAACTTGT	CAAATCTTTG	AAACTTGGAA	TATATTGCTT
901	TCATAATATG	AAGTTTTATT	GCCTATCTAT	CTGAAGTGTC	TATTTTTC
951	AGTTTGTAA	TTTATTATGT	GGTTTTAACA	TTGGGTGTTT	TTGTTTGT
1001	TTTACTATGA	AAAGACAGCT	TAAGGAAGAG	CTAAATTC	TTAAATATT
1051	TGGGGCATGT	TTGTGCACTG	CTGTTGTGAG	GATCAGCATA	TGAAATTGAC
1101	ATCATGGTTA	GTCATGGTAC	TGCAGCTTAG	GGGGCTACAC	GGTTGCTGTG
1151	TGAGTGGAGA	GATGCAGTGA	GGCAGTTGTC	ATTATTCTAA	AAATTGTACT
1201	ACTTTCACCT	TTCCCAAAGA	TTATATAATG	TTCATAATCC	ACCATGAAAA
1251	CAGCATTGGC	CAAAGGTACT	GAGGCTGCTT	AAAATATTCA	ATTCTGCTTT
1301	TTAGTTTTTA	AGTGAATTTA	GTTTGAAAAG	CATGATTATA	CAGGCCTCTC
1351	GAGGCTGAGT	GCTACTTTTCG	GTAAAGTTCC	AGTTTTCCAG	CCTTCTGTGA
1401	CAGGATGAAT	GAGGTGGGTA	TGGACAGTGG	AGGCAGCTGG	AATGGCAAGT
1451	GCAGAAAATA	GGAACAGTTC	TATACAGTGC	TCTCATTTAC	TAATAACATA
1501	ATGCCTTCTA	AATAATTTTT	TTGGGAAACT	ACATTATCAC	AAAAATTATAC
1551	AAATTTTTTT	ACAAGTATTT	ACATACTGTA	TCTGAAAACA	GACTTTAAAG
1601	TCACAAGATT	ATAAATGTAC	ATATGTATT	TCACATTCTG	AAAAATAACA
1651	TTCTCAGAAT	CCACAGAAAA	TATACTTAGT	TACTACTGAA	GATAATTTTT
1701	GAAATGTAAA	AATTAGATTT	AAATAGTATA	TTTTAAATGA	CAGAACTATA
1751	ATTACAGAGA	TCAGATCAGA	TAGGTAAACT	GCAAGATAGA	TAGGATGAAA
1801	CTTTTGGCCT	ACTGTATTAC	TTACAGAGTT	TTTTTGTGTG	TGGTTTTTAA
1851	AACTGTTAAG	GCAAGAAGTG	TCAAATGCTT	TAGAGTTAAA	TAACAGATCA
1901	CTGATTTCAA	AGACTTGGTG	TATAGTGTTA	AAAATTAAAG	CTTAAAGGT
1951	GGTTAGAAAA	GTGGATTAAT	GCAAAAGGGG	TAATAAAGAC	TGCAACATT
2001	TCAGGACCAA	ATTAAACTGC	T		

**Figure 20**

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1      EDDDYGSRTG SISSSVSVPA KPERRPSLPP SKQANKNLIL KAISEAQESV
51     TKTINYSTVP QKQTLPVAPR TRTSQEELLA EVVQGSRTTP RISPPIKEEE
101    TKGDSVEKNQ AEMSELSVAQ KPEKLLERCK YWPACKNGDE CAYHHPISPC
151    KAFPNCFAE KCLFVHPNCK YDAKCTKPDG PFTHVSRRIIP VLSPKPVAPP
201    APPSSSQLCR YFPACKMEC PFYHPKHCRF NTQCTSPDCT FYHPTINVPP
251    RHALKWIRPQ TSE•HPVLPG RRSCSLEVEM Y••KILYRTC QIFETWNILL
301    S•YEVLLPIY LKCLIFQVCK FIMWF•HWVF LFCFYYEKTA •GRAKFC•NI
351    WGMFVHCCCE DQHMCLTSWL VMVLQLRGLH GCCVSGEMQ• GSCHYSKNCT
401    TFTFPKDYIM FIIHHENSIG QRY•GCLKYS ILLFSF•VNL V•KA•LYRPL
451    EAECYFR•SS SFPAPCDRMN EVGMDSGGSW NGKCRK•EQF YTVLSFTNNI
501    MPSK•FFWET TLSQNYTNFF TSIYILYLKT DFKVTRL•MY ICILTF•KIT
551    FSESTENILS YY•R•FLKCK N•I•IVYFK• QNYNYRDQIR •VNCKIDRMK
601    LLAYCITYRV FLCVVFCTVK ARSVKCFRVK •QITDFKDLV YSVKN•SLKG
651    G•KSGLMQKG ••RLQHSQDQ IKL

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EDDDYGSRTG SISSSVSVPA KPERRPSLPP SKQANKNLIL KAISEAQESV
TKTINYSTVP QKQTLPVAPR TRTSQEELLA EVVQGSRTTP RISPPIKEEE
TKGDSVEKNQ AEMSELSVAQ KPEKLLERCK YWPACKNGDE CAYHHPISPC
KAFPNCFAE KCLFVHPNCK YDAKCTKPDG PFTHVSRRIIP VLSPKPVAPP
APPSSSQLCR YFPACKMEC PFYHPKHCRF NTQCTSPDCT FYHPTINVPP
RHALKWIRPQ TSE

```

**Figure 21**

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1      AAAACTTTCG GAAGAGAAAG TTGCCTGTGG TAAGTTCAGT TGTTAAAGTA
51     AAAAAATTCA ATCATGATGG AGAAGAGGAG GAAGAAGATG ATGATTACGG
101    GTCTCGAACA GGAAGCATCT CCAGCAGTGT GTCTGTGCCT GCAAAGCCTG
151    AAAGGAGACC TTCTCTTCCA CCTTCTAAAC AAGCTAACAA GAATCTGATT
201    TTGAAGGCTA TATCTGAAGC TCAAGAATCC GTAACAAAAA CAACTAACTA
251    CTCTACAGTT CCACAGAAAC AGACACTTCC AGTTGCTCCC AGAACTCGAA
301    CTTCTCAAGA AGAATTGCTA GCAGAAJTG G TCCAGGGGAC AAAGTAGGAC
351    CCCCAGAATA AGTCCCCCCA TTAAAGAAGA GGAAACAAAA GGAGATTCTG
401    TAGAAAAAAA TCAAGATTAC TATGACATGG AATCCATGGT CCATGCAGAC
451    ACAAGATCAT TTATTCTGAA GAAGCCAAAG CTGTCTGAGG AAGTANTAGT
501    GGCACCAAAC CAAGANTCGG GGATGAAGAC TGCAGATTCC CTTCGGGTTT
551    TTTCAAGGAC CCTTATGCAG ACACNAGATC TTGTTCAACC AGATAAACCT
601    GCAAGTCCCA AG

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1      KTFGRESCLW •VQLLK•KNS IMMEKRRKKM MITGLEQEAS PAVCLCLQSL
51     KGDLLFHLN KLTRI•F•RL YLKLKNP•QK QLTTLQFHRN RHFQLLEPEL
101    LLKKN•QKW SRGQSRTPRI SPPIKEEETK GDSVEKNQDY YMESMVHAD
151    TRSFILKKPK LSEEVXVAPN QXSGMKTADS LRVLSGTLMQ TXDLVQDPKP
201    ASPK

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1      NAGCTGCTCT GACGGGNAGN GGAATGNATG GNGGCTTGTT CNGAAACNNG
51     CCAGATGGCG NGAGGGGGAC AAGTAGCGGC GTGATTNAGA AGAGGGAGGT
101    GAGGGTNCTC ACATCACCNC ATCTNACCAT GNCNGGCCNT CCCCANTANT
151    AANANTGATG ATAGNGGGAA GTGGGCCAC CCAGAAGCNT GATTGAGCGG
201    CCGCCAGTAN GAAACNNGTT TGTCCANTTA GNCATACNNA TNGTAGGGTT
251    CNAGCNGCGT CCCCAGCACC NGCANANNNN CNNGCNGGGAC NACNGCCCN
301    NNNNTNGTTA NNCNGNGNAG NNAAAAAATT CAATCATGAT GGAGAAGAGG
351    AGGAAGAAGA TGATGATTAC GGGTCTCGAA CAGGAAGCAT CTCCAGCAGT
401    GTGCTGTGC CTGCAA

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Untitled translated in RF 2

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1      SCSDGXXNXW XLVXXKARWX EGDK•RRDXE EGGEGXHITX SXHXXSPXX
51     XXMXGSGPT QKXD•AAASX KXVCPXHXK XRVXXASPAX AXXXXGXKPX
101    XXLXXXXKKF NHDGEEEEED DDYGSRTGSI SSSVSVPA

```

**Figure 22****CH1-9a11-2**

GA AAA CAA ATG GAA GAA ATG CAA AAG GCT TTC AAT AAA ACA ATC GTG  
 AAA CTT CAG AAT ACT TCA AGA ATA GCA GAG GAG CAG GAT CAG CGG CAA  
 ACT GAA GCC ATC CAG TTG CTA CAG GCA CAG CTG ACC AAC ATG ACA CAG  
 CTT GTT CAA

Lys Gln Met Glu Glu Met Gln Lys Ala Phe Asn Lys Thr Ile Val Lys  
 Leu Gln Asn Thr Ser Arg Ile Ala Glu Glu Gln Asp Gln Arg Gln Thr  
 Glu Ala Ile Gln Leu Leu Gln Ala Gln Leu Thr Asn Met Thr Gln Leu  
 Val Gln

**CH8-2a13-1**

GAA CAG GCA AGC AGA TAT GCT ACT GTC AGT GAA AGA GTG CAT GCT CAA  
 GTG CAG CAA TTT CTA AAA GAA GGT TAT TTA AGG GAG GAG ATG GTT CTG  
 GAC AAT ATC CCA AAG CTT CTG AAC TGC CTG AGA GAC TGC AAT GTT GCC  
 ATC CGA TGG CTG ATG CTT C

Glu Gln Ala Ser Arg Tyr Ala Thr Val Ser Glu Arg Val His Ala Gln  
 Val Gln Gln Phe Leu Lys Glu Gly Tyr Leu Arg Glu Glu Met Val Leu  
 Asp Asn Ile Pro Lys Leu Leu Asn Cys Leu Arg Asp Cys Asn Val Ala  
 Ile Arg Trp Leu Met Leu

**CH13-2a12-1**

CTC ACA ATG GGC TAC TGG CCA ACA TAC ACG CCC ATG GAA GTG CAC TTA  
 ACC CCA GAA ATG ATT AAA CTT CAG GAA GTA TTT AAG GCA TTT TAT CTT  
 GGA AAG CAC AG

Leu Thr Met Gly Tyr Trp Pro Thr Tyr Thr Pro Met Glu Val His Leu  
 Thr Pro Glu Met Ile Lys Leu Gln Glu Val Phe Lys Ala Phe Tyr Leu  
 Gly Lys His

**CH14-2a16-1**

TG TTT GTT CAC CCA AAT TGT AAA TAT GAT GCA AAG TGT ACT AAA CCA  
 GAT TGT CCC TTC ACT CAT GTG AGT AGA AGA ATT CCA GTA CTG TCT CCA  
 AAA CCA GTT GCA CCA CCA G

Phe Val His Pro Asn Cys Lys Tyr Asp Ala Lys Cys Thr Lys Pro Asp  
 Cys Pro Phe Thr His Val Ser Arg Arg Ile Pro Val Leu Ser Pro Lys  
 Pro Val Ala Pro Pro

**Figure 23(A)**

```

CTCAGAGAGG GCTGCCAGGA CGCGAGCCAC TGAGGAGCCG CTCAGCCAGC
GCCATAGCCC TTAGGACTAT CGGTCACATT CTCGCGCTCC TGCTCCGGCT
CCTCCATCTT GGCCTCGGCA GTGGCGGCTG CCGGGAGGAT GTGCCGCCTT
CTGGCAGGGG GAAGAAGGAG GAGAAGATGA AGAAGCACCG GCGGGCCTTG
GCCCTGGTCT CCTGCCTCTT TCTGTGCTCT CTGGTCTGGC TTCCCAGCTG
GCGTGTATGT TGTAAGAGA GTTCCTCAGC TTCAGCGTCA TCATATTACT
CTCAAGATGA CAACTGCGCA CTAGAAAATG AAGATGTACA ATTCCAGAAA
AAGAATACAG AGTCAAAAAA GTTAAGTCCA CCGGTGGTGG AGACACTCCC
TACAGTTGAT TTGCATGAAG AGTCTTCCAA TGCAGTTGTG GACAGTGAAA
CTGTTGAAAA TATTTCCAGC TCATCTACCT CAGAAATCAC TCCAATCTCA
AAGCTTGATG AAATAGAAAA ATCTGGTACT ATTCCGATAG CCAAACCAAG
TGAACTGAG CAGTCTGAAA CTGATTGTGA TGTGGTGAG GCCCTTGATG
CTAGTGCTCC AATTGAACAA CCTTCCTTTG TCAGTCCACC TGACAGCCTT
GTTGGCCAGC ATATAGAAAA TGTATCATCT TCACATGGTA AAGGAAAGAT
AACAAAATCA GAATTTGAAT CAAAAGTTTC AGCAAGTGAA CAGGGCGGTG
GTGATCCAAA ATCTGCATTG AATGCTTCAG ATAATTTAAA AAATGAGAGC
TCTGATTATA CAAAACCAGG AGACATTGAC CCTACATCAG TAGCAAGTCC
CAAAGATCCA GAAGATATAC CAACATTTGA TGAATGGAAG AAGAAAGTTA
TGGAAGTAGA AAAAGAAAAA AGTCAGTCGA TGCATGCATC TTCTAATGGA
GGTTCACATG CCACCAAAAA GGTCCAGAAA AATCGAAATA ATTATGCCTC
AGTAGAATGT GGTGCCAAAA TTCTAGCAGC TAATCCAGAA GCCAAGAGCA
CATCTGCTAT TCTTATAGAA AATATGGATC TTTACATGTT GAATCCTTGC
AGCACTAAAA TTTGGTTTGT TATTGAACTT TGTGAACCAA TTCAAGTAAA
ACAGCTTGAT ATTGCAAATT ATGAATTATT TTCTTCTACT CCTAAAGATT
TTCTGGTTTC TATCAGTGAC AGATATCCAA CAAATAAGTG GATTAAGCTG
GGTACTTTTC ATGGTAGAGA TGAGCGGAAT GTACAGAGTT TCCCTTTAGA
TGAACAGATG TATGCAAAAT ATGTCAAGGT TGAGTTGCTA TCACATTTTG
GATCAGAGCA CTTTTGTCCA TTAAGCCTTA TAAGGGTATT TGGCACTAAC
ATGGTGGAAG AATATGAAGA AATTGCTGAT TCCCAGTATC ACTCAGAACC
CCAGGAAC TAATGATGAGG ACTATGATTA TCCACTGGAT TATAATACTG
GAGAGGATAA ATCCTCAAAA AATCTTCTTG GTTCTGCTAC AAATGCCATT
CTAAATATGG TGAATATTGC TGCTAATATT CTGGGAGCAA AAATGAAGA
CCTGACAGAA GGAAATAAAA GTATATCTGA GAATGCCACT GCCACAGCTG
CACCTAAAAT GCCTGAATCA ACTCCTGTTT CAACTCCTGT TCCATCTCCT
GAGTATGTAA CCACTGAAGT ACACACACAT GACATGGAGC CGTCAACACC
AGATACTCCA AAAGAGAGTC CCATTGTACA GTTAGTTCAA GAGGAGGAAG
AGGAGGCAAG TCCATCTACA GTGACCCTTC TGGGCAGCGG TGAACAGGAA
GATGAATCAT CACCCTGGTT TGAGTCAGAG ACACAAATAT TTTGCAGTGA

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**Figure 23(B)**

ACTGACCACA ATTTGTTGTA TTTCTAGTTT TTCAGAATAC ATATATAAAT  
 GGTGTTTCAGT TAGAGTTGCT CTTTATCGGC AGCGCAGCCG AACTGCTTTG  
 AGTAAAGGAA AAGATTATCT TGTGTTAGCT CAACCACCCT TACTACTTCC  
 TGC GGAATCA GTAGATGTTT CAGTATTGCA ACCTCTGAGT GGAGAATTGG  
 AAAATACGAA TATAGAAAGG GAAGCTGAAA CTGTTGTTCT GGGTGATTTA  
 AGTAGTAGTA TGCACCAGGA TGACTTGGTG AATCACACTG TAGATGCAGT  
 TGAAGTTGAA CCAAGCCATT CTCAAACCTCT TTCTCAGTCT CTTCTTTTAG  
 ATATTACCCC AGAAATCAAT CCCTTGCCTA AAATAGAAGT ATCTGAGTCT  
 GTTGAATATG AGGCAGGACA TATACCATCA CCAGTGATTG CCCAAGAGAG  
 TTCTGTTGAG ATCGATAATG AAACAGAACA AAAGTCTGAG AGCTTTAGTT  
 CTATAGAGAA ACCATCTATT ACCTATGAAA CAAATAAAGT TAATGAGTTA  
 ATGGATAATA TTATAAAAGA AGATATGAAC TCCATGCAAA TTTTCACAAA  
 GCTGTCTGAA ACAATAGTGC CACCAATAAA TACAGCCACT GTACCCGACA  
 ATGAAGATGG GGAAGCCAAA ATGAATATAG CTGACACAGC AAAGCAAAC  
 TTGATTTCTG TTGTGGATTG TTCTTCATTA CCTGAAGTAA AAGAAGAAGA  
 ACAGTCTCCA GAAGATGCCC TTTTGAGAGG GTTACAGAGG ACAGCTACAG  
 ATTTTATGCT GAATTGCAA AATTCTACAG ATCTAGGATA TGCTAATGGA  
 AATCTTGATC ATGGATCAAA CCAAAGGAG TCAGTATTTA TGAGACTTAA  
 TAATCGTATT AAAGCCTTAG AAGTTAACAT GTCTCTCAGT GGTGCTATC  
 TGGAGGAGCT TAGCCAAAGG TACCGAAAAC AAATGGAAGA AATGCAAAAG  
 GCTTTCAACA AAACAATCGT GAAACTTCAG AATACTTCAA GAATAGCAGA  
 GGAGCAGGAT CAGCGGCAAA CTGAAGCCAT CCAGTTGCTA CAGGCACAGC  
 TGACCAACAT GACACAGCTT GTTTCAAATT TATCAGCAAC AGTAGCAGAA  
 TTGAAACGGG AGGTTTCAGA TCGACAAAGC TATCTTGTC TATCTTTGGT  
 TCTTTGTGTT GTCTTGGGAC TGATGCTTTG TATGCAGCGT TGTCGAAATA  
 CTTCTCAATT TGATGGAGAT TATATTTCAA AACTTCTTAA AAGTAATCAG  
 TATCCAAGCC CTAAAAGGTG TTTCTCTTCC TATGATGATA TGAATTTGAA  
 AAGAAGAAGT TCATTCCCAC TCATGAGATC CAAGTCTCTA CAGTTAACTG  
 GCAAAGAAGT AGACCCAAAT GATTTGTACA TTGTAGAACC CCTCAAGTTT  
 TCTCCAGAAA AGAAGAAGAA GCGCTGCAAG TACAAAATTG AAAAAATTGA  
 GACCATAAAG CCTGAAGAAC CATTGCACCC CATAGCCAAT GGCGACATAA  
 AAGGAAGAAA GCCCTTTACG AACCAGAGAG ATTTTCTTAA TATGGGAGAA  
 GTTTATCACT CTTCTTATAA AGGTCCTCCA TCTGAAGGAA GCTCAGAAAC  
 TTCATCACAG TCAGAAGAGT CCTATTTTTG TGGCATTTC GCTTGACAA  
 GTCTGTGCAA TGGACAGTCT CAAAAGACAA AAAGTGAAG GAGGGCTTTA  
 AAACGAAGAC GATCTAAAGT CCAAGACCAA GGAAAATTGA TAAAACTCT  
 AATACAGACT AAGTCGGGAT CATTGCCGAG CCTGCATGAC ATAATCAAAG  
 GAAACAAAGA GATCACCGTG GGAACATTTG GTGTTACAGC AGTCTCGGGA

**Figure 23(C)**

CATATCTAAA ATTAATTGAA CTTTTCATAC AGAAGACTTT TTTGTTGTTG  
TTCTTTGAAG AACAGTCTGT AGTATTTGAA GGGTTTGGGG GAGGGAGAAA  
ATATTAATGG GAAAGGCATT CAGAAATTAT GGTTTCTACC TTTTAAAAA  
GTAGATGGGA TTGTGCTCAA TCTTGGTTAA TGAGCTACAG TTTTACAAAG  
CTGATCACTT CCTATAAGGA CAATGGTAGA CATTTTATAA AGATGTTTTT  
TCACAAGATT AATTACTGGG ACAAAGTAA TTTGGAAGCC CAGTTCCTTA  
GGTGGGATAG GAATGAAAGC CTAAACCTCT TCCTTTAGCT TTGTTCCCTAT  
TTCTTGCACC TTCCCATATT TATGTGCCTT TTGTCTATTT ATAATGCCAC  
TGGAAGAGGA GGGATAACTT TTTCTGTTAT TTGATTTCTT TTATAACTTT  
GTTAGGTTTT TGAAGCTGCA AACACTACAA TGCTTTGAGG GGGTCTGTGC  
CTGAAGCTCA GGAGTGTGGA TCAGACAGTC TAAAGATCCT AAAAAGTTGC  
CAACTGGATC TTTGTTTAGC AAACCTCACTG GAAATGAACA CTTAATGGAA  
TTTTTAAGTC TGTTCGTGTA GGTAGATGGT GATGCTCTTG TTATTTTCAC  
TTATTCAGGC TGGATTACTT CTTACTTAGT TACTAACTCA ATGAGGAAAA  
AATCCCTACA GGATCTTTTT TTGCAAACAA CTGATATATG CAGACAAATT  
TTTGACAAAT TCACCTTTTA AACACGACGT TAACCGATTT GTGAAGGTTT  
TCTTTAGCTT ACATTTTAAA CATACACAAT AAACACTAAT CCTCCAAACT  
TTCACTGTTT TTATTAGTAT GAATATAAAA TTTGAAGGTT TGGCCAATTA  
GTACAAGTCT CATGATATAA TCACAGCCTG CATACATATG CACAGATCCA  
GTTAGTGAGT TTGTCAAGCT TAATCTAATT GGTTAAGTCT AAAGAGATTA  
TTATTCCTTG ATGTTTGCTT TGTATTGGCT ACAAATGTGC AGAGGTAATA  
CATATGTGAT GTCGATGTCT CTGTCTTTTT TTTTGTCTTT AAAAATAAT  
TGGCAGCAAC TGTATTTGAA TAAAATGATT TCTTAGTATG ATTGTACAGT  
AATGAATGAA AGTGGAACAT GTTCTTTTTT GAAAGGGAGA GAATTGACCA  
TTTATTGTTG TGATGTTTAA GTTATAACTT ATTGAGCACT TTTAGTAGTG  
ATAACTGTTT TTAAACTTGC CTAATACCTT TCTTGGGTAT TGTTTGTAAT  
GTGACTTATT TAACGCCTTC TTTGTTTGTT TAAGTTGCTG CTTTAGGTTA  
ACAGCGTGTT TTAGAAGATT TAAATTTCTT TCCTGTCTGC ACAATTAGCT  
ATTCAGAGCA AGAGGGCCTG ATTTTATAGA AGCCCTTGA AAAGAGGTCC  
AGATGAGAGC AGAGATACAG TGAGAAATTA TGTGATCTGT GTGTTGTGGG  
AAGAGAATTT TCAATATGTA ACTACGGAGC TGTAGTGCCA TTAGAACTG  
TGAATTTCCA AATAAATCTG AACACTTGTC TTTATT

**Figure 24**

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QRGLPGREPL RSRASAIAL RTIGHILALL LRLHLGLGS GGCREDPVPS
GRGKKEEKMK KHRRALALVS CLFLCSLVWL PSWRVCKES SSASASSYYS
QDDNCALENE DVQFQKKNTE SKKLSPPVVE TLPTVDLHEE SSNAVVDSET
VENISSSTS EITPISKLE IEKSGTIPIA KPSETEQSET DCDVGEALDA
SAPIEQPSFV SPPDSL VGQH IENVSSSHGK GKITKSEFES KVSASEQGGG
DPKSALNASD NLKNESDYT KPGDIDPTSV ASPKDPEDIP TFDEWKKKVM
EVEKEKSQSM HASSNGGSHA TTKVQKNRNN YASVECGAKI LAANPEAKST
SAILIENMDL YMLNPCSTKI WFVIELCEPI QVKQLDIANY ELFSSTPKDF
LVSISDRYPT NKWIKLGTFFH GRDERNVQSF PLDEQMYAKY VKVELLSHFG
SEHFCPLSLI RVFGTNMVEE YEEIADSQYH SERQELFDED YDYPLDYNTG
EDKSSKNLLG SATNAILNMV NIAANILGAK TEDLTEGNKS ISENATATAA
PKMPESTPVS TPVPSPEYVT TEVHTHDMEP STPDTPKESP IVQLVQEEEE
EASPSTVTLL GSQEQEDESS PWFESQTIF CSELTICCI SSFSEYIYKW
CSVRYALYRQ RSRTALSKGK DYLVLAQPPL LLPAESVDVS VLQPLSGELE
NTNIEREAET VVLGDLSSSM HQDDLNVHTV DAVELEPSHS QTLQSLLLD
ITPEINPLPK IEVSESVEYE AGHIPSPVIP QESSVEIDNE TEQKSESFSS
IEKPSITYET NKVNELMDNI IKEDMNSMQI FTKLSETIVP PINTATVPDN
EDGEAKMNIA DTAKQTLISV VDSSSLPEVK EEEQSPEDAL LRGLQRTATD
FYAELQNSTD LGYANGNLVH GSNQKESVFM RLNNRIKALE VNMSLSGRYL
EELSQRYSRQ MEEMQKAFNK TIVKLQNTSR IAEEQDQRQT EAIQLLQAQL
TNMTQLVSNL SATVAELKRE VSDRQSYLVI SLVLCVVLGL MLMQRCRNT
SQFDGDYISK LPKSNQYPSK KRCFSSYDDM NLKRRTSFPL MRSKSLQLTG
KEVDPNDLYI VEPLKFSPEK KKKRCKYKIE KIETIKPEEP LHPIANGDIK
GRKPFTNQRD FSNMGEVYHS SYKGPPSEGS SETSSQSEES YFCGISACTS
LCNGQSQKTK TEKRALKRRR SKVQDQGKLI KTLIQTKSGS LPSLHDIKG
NKEITVGTFG VTAVSGHI•N •LNFSYRRLF CCCSLKNSL• YLKGLGEGEN
INGKGIQKLW FLPF•KVDGI VLNLG••ATV LQS•SLPIRT MVDIL•RCFF
TRLITGTVKI WKPSSLGGIG MKA•TSSFSF VPISCTFPYL CAFCLFIMPL
EEEG•LFLLF DFFYNFVRFL KLQTLQCFEG VCA•SSGVWI RQSKDPKNLP
TGSFLSKLTG NEHLMEFLSL FC•VDGDALV IFTYSGWITS YLVTNSMRKK
SLQDLFLQTT DICRQIFDKF TF•TRR•PIC EGFL•LTF•T YTINTNPPNF
HCFY•YKEYI •RFGQLVQVS •YNHSLHTYA QIQLVSLSSL I•LVKSKEII
IP•CLLCIGY KCAEVIHM•C RCLCLFFCL• KIIGSNCI•I K•FLSMIVQ•
•MKVEHVSF• KGEN•PFIVV MFKL•LIEHF ••••LFLNLP NTFLGYCL•C
DLFNAFFVCL SCCFRLTACF RRFKFLSCLH N•LFRARGPD FIEAP•KEVQ
MRAEIQ•EIM •SVCCGKRIF NM•LRSCSAI RNCEFPNKSE HLST

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**Figure 25(A)**

```

TAGAATTCAG CGGCCGCTGA ATTCTAGCTG CGGGGTAGGA GTCCGCGGCA
GCCTCCGGGT AAGCCAAGCG CCGCGCAGTG CTGAGTTCCC GCACGCCGCA
GAGCCATGGA GATCGGCACC GAGACCAGCC GCAAGATCCG GAGTGCCATT
AAGGGGAAAT TACAAGAATT AGGAGCTTAT GTTGATGAAG AACTTCCTGA
TTACATTATG GTGATGGTGG CCAACAAGAA AAGTCAGGAC CAAATGACAG
AGGATCTGTC CCTGTTTCTA GGAACAACA CAATTCGATT CACCGTATGG
CTTCATGGTG TATTAGATAA ACTTCGCTCT GTTACAACCTG AACCTCTAG
TCTGAAGTCT TCTGATACCA ACATCTTTGA TAGTAACGTG CCTTCAAACA
AGAACAATTT CAGTCGGGGA GATGAGAGGA GGCATGAAGC TGCAGTGCCA
CCACTTGCCA TTCCTAGCGC GAGACCTGAA AAAAGAGATT CCAGAGTTTC
TACAAGTTTC CAGGAGTCAA AAACCACAAA TGTCAGACAG ACTTACGATG
ATGGAGCTGC AACCCGACTA ATGTCAACAG TGAAACCTTT GAGGGAGCCA
GCACCCTCTG AAGATGTGAT TGATATTAAG CCAGAACCAG ATGATCTCAT
TGACGAAGAC CTCAACTTTG TGCAGGAGAA TCCCTTATCT CAGAAAGAAC
CTACAGTGAC ACTTACATAT GGTTCTTCTC GCCCTTCTAT TGAAATTTAT
CGACCACCTG CAAGTAGAAA TGCAGATAGT GGTGTTTCATT TAAACAGGTT
GCAATTTCAA CAGCAGCAGA ATAGTATTCA TGCTGCCAAG CAGCTTGATA
TGCAGAGTAG TTGGGTATAT GAAACAGGAC GTTTGTGTGA ACCAGAGGTG
CTTAACAGCT TAGAAGAAAC GTATAGTCCG TTCTTTAGAA ACAACTCGGA
GAAAATGAGT ATGGAGGATG AAAACTTTTCG GAAGAGAAAG TTGCCTGTGG
TAAGTTCAGT TGTTAAAGTA AAAAAATTCA ATCATGATGG AGAAGAGGAG
GAAGGAGATG ATGATTACGG GTCTCGAACA GGAAGCATCT CCAGCAGTGT
GTCTGTGCCT GCAAAGCCTG AAAGGAGACC TTCTCTTCCA CCTTCTAAAC
AAGCTAACAA GAATCTGATT TTGAAGGCTA TATCTGAAGC TCAAGAATCC
GTAACAAAAA CAACTAACTA CTCTACAGTT CCACAGAAAC AGACACTTCC
AGTTGCTCCC AGAACTCGAA CTTCTCAAGA AGAATTGCTA GCAGAAGTGG
TCCAGGGACA AAGTAGGACC CCCAGAATAA GTCCCCCAT TAAAGAAGAG
GAAACAAAAG GAGATTCTGT AGAAAAAAAT CAAGCTGAGA TGAGTGAAC
GAGTGTGGCA CAGAAACCAG AAAAATTTT GGAGCGCTGC AAGTACTGGC
CTGCTTGTA AAATGGGGAT GAGTGTGCCT ACCATCACCC CATCTCACCC
TGCAAAGCCT TCCCCAATTG TAAATTTGCT GAAAAATGTT TGTTTGTTCA
CCCAAATTGT AAATATGATG CAAAGTGTAC TAAACCAGAT TGTCCCTTCA
CTCATGTGAG TAGAAGAATT CCAGTACTGT CTCCAAAACC AGTTGCACCA
CCAGCACCAC CTTCCAGTAG TCAGCTCTGC CGTTACTTCC CTGCTTGTA
GAAGATGGAA TGTCCCTTCT ATCATCCAAA ACATTGTAGG TTAAACACTC
AATGTACAAG TCCGGACTGC ACATTCTACC ATCCCACCAT TAATGTCCCA
CCACGACATG CCTTGAAATG GATTCGACCT CAAACCAGCG AATAGCACCC
AGTCCTGCCT GGCAGAAGAT CATGCAGTTT GGAAGTTTTT ATGTACTGAT

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**Figure 25(B)**

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GAAAGATACT CTACAGAACT TGTCAAATCT TTGAAACTTG GAATATATTG
CTTTCATAAT ATGAAGTTTT ATTGCCTATC TATCTGAAGT GTCTAATTTT
TCAAGTTTGT AAGTTTATTA TGTGGTTTTA ACATTGGGTG TTTTGTTTT
GTTTTTACTA TGAAAAGACA GCTTAAGGAA GAGCTAAATT CTGTTAAAAT
ATTTGGGGCA TGTGTGTGCA CTGCTGTTGT GAGGATCAGC ATATGAAATT
GACATCATGG TTAGTCATGG TACTGCAGCT TAGGGGGCTA CACGGTTGCT
GTGTGAGTGG AGAGATGCAG TGAGGCAGTT GTCATTATTC TAAAAATTGT
ACTACTTTCA CTTTTCCCAA AGATTATATA ATGTTCATAA TCCACCATGA
AAACAGCATT GGCCAAAGGT ACTGAGGCTG CTTAAAATAT TCAATTCTGC
TTTTTAATTT TTAAGTGAAT TTAGTTTGAA AAGCATGATT ATACAGGCCT
CTCAGGCTGA GTGCTACTTT CGGTAAAGTT CCAGTTTTCC TGCCTTCTGT
GACAGGATGA ATGAGGTGGG TATGGACAGT GGAGGCAGCT GGAATGGCAA
GTGCAGAAAA TAGGAACAGT TCTATACAGT GCTCTCATTT ACTAATAACA
TAATGCCTTC TAAATAATTT TTTTGGGAAA CTACATTATC ACAAATTTAT
ACAAATTTTT TTACAAGTAT TTACATACTG TATCTGAAAA CAGACTTTAA
AGTCACAAGA TTATAAATGT ACATATGTAT TCTCACATTC TGAAAAATAA
CATTCTCAGA ATCCACAGAA AATATACTTA GTTACTACTG AAGATAATTT
TTGAAATGTA AAAATTAGAT TTAAATAGTA TATTTTAAAT GACAGAACTA
TAATTACAGA GATCAGATCA GATAGGTAAA CTGCAAGATA GATAGGATGA
AACTTTTGGC CTACTGTATT ACTTACAGAG TTTTTTTGTG TGTGGTTTTT
AAAAGTGTTA AGGCAAGAAG TGTCAAATGC TTTAGAGTTA AATAACAGAT
CACTGATTTT AAAGACTTGG TGTATAGTGT TAAAAATTAA AGCTTAAAAG
GTGGTTAGAA AAGTGGATTA ATGCAAAAGG GGTAATAAAG ACTGCAACAT
TCTCAGGACC AAATTAACT GCTAA
```

**Figure 26**

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•NSAAAEF•L RGRSPRQPPG KPSAAQC•VP ARRRAMEIGT ETSRKIRSAI
KGKLQELGAY VDEELPDYIM VMVANKKSQD QMTEDLSLFL GNNTIRFTVW
LHGVLDKLRS VTTEPSSLKS SDTNIFDSNV PSNKNNFSRG DERRHEAAVP
PLAIP SARPE KRDSRVSTSS QESKTTNVRQ TYDDGAATRL MSTVKPLREP
APSEDVIDIK PEPDDLIDED LNFVQENPLS QKEPTVTLTY GSSRPSIEIY
RPPASRNADS GVHLNRLQFQ QQQNSIHA AK QLDMQSSWVY ETGRLCEPEV
LNSLEETYS P FFRNNSEKMS MEDENFRKRK LPVVSSVVKV KKFNDGEEEE
EGDDDYGSRT GSISSSVSVP AKPERRPSLP PSKQANKNLI LKAISEAQES
VTKTTNYSTV PQKQTL PVAP RTRTSQEELL AEVVQGSRT PRISPIKEE
ETKGDSVEKN QAEMSELSVA QKPEKLLERC KYWPACKNGD ECAYHHPISP
CKAFPNC KFA EKCLFVHPNC KYDAKCTKPD CPFTHVSRRI PVLSPKPVAP
PAPPSSSQLC RYFPACKKME CPFYHPKHCR FNTQCTSPDC TFYHPTINVP
PRHALKWIRP QTSE•HPVLP GRRSCSLEVF MY••KILYRT CQIFETWNIL
LS•YEVLLPI YLKCLIFQVC KFIMWF•HWV FLFCFYYEKT A•GRAKFC•N
IWGMFVHCCC EDQHMKLTSW LVMVLQLRGL HGCCVSGEMQ •GSCHYSKNC
TTFTFPKDYI MFIIHHENSI GQRY•GCLKY SILLFNF•VN LV•KA•LYRP
LRLSATFGKV PVFLPSVTG• MRWVWTVEAA GMA SAENRNS SIQCSHLLIT
•CLLNNFFGK LHYHKIIQIF LQVFTYCI•K QTLKSQDYKC TYVFSHSEK•
HSQNPQKIYL VTTEDNF•NV KIRFK•YILN DRTIITEIRS DR•TAR•IG•
NFWPTVLLTE FFCVWFLKLL RQEVSNAL EL NNRSLISK TW CIVLKIK A•K
VVRKVD•CKR GNKDCNILRT KLNC•

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MEIGT ETSRKIRSAI
KGKLQELGAY VDEELPDYIM VMVANKKSQD QMTEDLSLFL GNNTIRFTVW
LHGVLDKLRS VTTEPSSLKS SDTNIFDSNV PSNKNNFSRG DERRHEAAVP
PLAIP SARPE KRDSRVSTSS QESKTTNVRQ TYDDGAATRL MSTVKPLREP
APSEDVIDIK PEPDDLIDED LNFVQENPLS QKEPTVTLTY GSSRPSIEIY
RPPASRNADS GVHLNRLQFQ QQQNSIHA AK QLDMQSSWVY ETGRLCEPEV
LNSLEETYS P FFRNNSEKMS MEDENFRKRK LPVVSSVVKV KKFNDGEEEE
EGDDDYGSRT GSISSSVSVP AKPERRPSLP PSKQANKNLI LKAISEAQES
VTKTTNYSTV PQKQTL PVAP RTRTSQEELL AEVVQGSRT PRISPIKEE
ETKGDSVEKN QAEMSELSVA QKPEKLLERC KYWPACKNGD ECAYHHPISP
CKAFPNC KFA EKCLFVHPNC KYDAKCTKPD CPFTHVSRRI PVLSPKPVAP
PAPPSSSQLC RYFPACKKME CPFYHPKHCR FNTQCTSPDC TFYHPTINVP
PRHALKWIRP QTSE

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